

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 11:31:07 ; Search time 81 Seconds  
(without alignments)  
761.746 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854  
Sequence: 1 MASTSYDYCRVPMEDGDKRC.....YFPSSQSSSAAPQLITVL 172

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23sep04:\*  
1: geneeqp1980s:\*  
2: geneeqp1990s:\*  
3: geneeqp2000s:\*  
4: geneeqp2001s:\*  
5: geneeqp2002s:\*  
6: geneeqp2003as:\*  
7: geneeqp2003bs:\*  
8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	854	100.0	180	2	AAR72703 Human mem
2	854	100.0	180	2	AAW65771 Protein r
3	854	100.0	180	2	AAW62207 Humantised
4	854	100.0	180	2	AAV02576 HML.24 an
5	854	100.0	180	2	AAV32765 Soluble H
6	854	100.0	180	2	AAV33202 Human HML
7	854	100.0	180	2	AAV05484 Potential
8	854	100.0	180	2	AAV07250 BST-2 pro
9	854	100.0	180	3	AAV53273 Human HML
10	854	100.0	180	4	AAV70697 Human HML
11	854	100.0	180	4	ABBS0295 Bone matr
12	854	100.0	180	5	ABBS3492 Human Bon
13	854	100.0	180	5	ABP35348 Human HML
14	854	100.0	180	5	ABP61469 Human NF-
15	854	100.0	180	5	AAW52356 Human HML
16	854	100.0	180	6	ABG71944 Human HML
17	854	100.0	180	6	ABG71944 Human HML
18	854	100.0	180	6	ABR92056 Human cer
19	854	100.0	180	6	ABU04150 Human exp
20	854	100.0	180	6	ABU04167 Human exp
21	854	100.0	180	6	ABU04162 Human exp
22	854	100.0	180	6	ABU04149 Human exp
23	854	100.0	180	6	ABU04154 Human exp
24	854	100.0	180	6	ABU04158 Human exp
25	854	100.0	180	6	ABU04168 Human exp

26	854	100.0	180	6	ABU04155 Human exp
27	854	100.0	180	6	ABU04157 Human exp
28	854	100.0	180	6	ABU04152 Human exp
29	854	100.0	180	6	ABU04166 Human exp
30	854	100.0	180	7	ADC38688 Human sec
31	854	100.0	180	7	ADP76564 Novel hum
32	854	100.0	180	8	ADJ75364 Cervical
33	854	100.0	180	8	ADL70569 Cervical
34	854	100.0	180	8	ADP60012 HML.24 ex
35	854	100.0	180	8	ADP07793 Human sec
36	854	100.0	180	8	ADP07794 Human sec
37	854	100.0	180	8	ADP07817 Human sec
38	854	100.0	180	8	ADP07764 Human sec
39	854	100.0	180	8	ADP07786 Human col
40	854	100.0	193	4	AAV73947 Human exp
41	854	100.0	193	6	ABU04151 Human exp
42	847	99.2	180	2	AAW77292 Protein b
43	847	99.2	180	6	ABU04156 Human exp
44	846	99.1	199	8	ADP07800 Human sec
45	834	97.7	178	8	ADJ67608 Human ova

# ALIGNMENTS

RESULT 1  
ID AAR72703 standard; protein; 180 AA.  
XX XX  
AC AAR72703;  
XX XX  
DT 25-MAR-2003 (revised)  
DT 06-DEC-1995 (first entry)  
XX XX  
DE Human membrane polypeptide for enhancing pre-B cell growth.  
XX XX  
KW Rheumatoid arthritis; diagnosis; pre-B cell growth; enhancement.  
XX XX  
OS Homo sapiens.  
XX XX  
PN WO9510536-A1.  
XX XX  
PD 20-APR-1995.  
XX XX  
PP 14-OCT-1994; 94MO-JP001732.  
XX XX  
PR 15-OCT-1993; 93JP-00281622.  
XX XX  
PA (HIRA/) HIRANO T.  
XX XX  
PI Hirano T, Kaisho T;  
XX XX  
DR WPI, 1995-161738/21.  
XX XX  
DR N-PSDB; AAQ89606.  
PT Recombinant membrane protein enhancing pre-B cell growth - and monoclonal  
PT antibody recognising it and useful in the diagnosis of rheumatoid  
PT arthritis.  
PT  
PS Claim 1; Page 29-30; 40pp; Japanese.  
XX XX  
CC A membrane polypeptide has been isolated from rheumatoid arthritis  
CC patients. The polypeptide supports pre-B-cell growth and is useful as an  
CC antigen for generating monoclonal antibodies for diagnosing rheumatoid  
CC arthritis. (Updated on 25-MAR-2003 to correct PN field.)  
XX XX  
SQ Sequence 180 AA;  
Query Match 100.0%; Score 854; DB 2; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6; 9e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASTSYDYCRVPMEDGDKRCLLLGILVLLITVLIVLPILFTIKNSACRDLRAV 60

DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
 QY 61 MECAVNTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELEGEI 120  
 DB 61 MECAVNTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELEGEI 120  
 QY 121 TTNHKLQDASAEVERLERRENOVLSVRIDAKKYPPSSODSSAAAPOLLIVL 172  
 DB 121 TTNHKLQDASAEVERLERRENOVLSVRIDAKKYPPSSODSSAAAPOLLIVL 172

RESULT 2  
 ID AAM65771 standard; protein; 180 AA.  
 AC AAM65771;  
 DT 20-NOV-1998 (first entry)

DE Protein recognised by anti-human HML.24 antibody.  
 XX Cytotoxic antibody; anti-human HML.24; lymphocytic tumours;  
 KM pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.  
 XX Homo sapiens.

OS MO9835698-A1.  
 PN 20-AUG-1998.  
 PD 12-FEB-1998; 98WO-JP000568.  
 PF 12-FEB-1997; 97JP-00041410.  
 PR 12-FEB-1997; 97JP-00041410.

XX (CHUS) CHUGAI SEIYAKU KK.  
 XX Kohshihara Y, Yoshimura Y;  
 PI MPI: 1998-456869/39.  
 DR N-PSDB; AAV07579.

PT Treatment of lymphocytic tumours using cytotoxic antibody - binding to  
 PT specific antigen such as HML.24 and effective against T-cell tumours and  
 PR B-cell tumours other than myeloma.

PS Claim 1; Page 44-45; 82pp; Japanese.

XX The protein having the amino acid sequence below is bound specifically by  
 CC a cytotoxic antibody which can be used in the treatment of lymphocytic  
 CC tumours, including T-cell tumours and B-cell tumours other than myeloma.  
 CC The antibody is preferably monoclonal and has AACC or CDC type  
 CC cytotoxicity. It may be chimeric or humanised, and preferably contains a  
 CC human antibody constant region C gamma (such as C gamma 1 or C gamma 3).  
 CC A preferred antibody is an anti-human HML.24 antibody or an antibody  
 CC which binds to an epitope recognising anti-human HML.24 antibody. The  
 CC cytotoxic antibody is useful in the treatment of lymphocytic tumours such  
 CC as acute or chronic B lymphocytic leukaemia, pre-B lymphoma, Burkitt's  
 CC lymphoma, or acute or chronic T lymphocytic leukaemia

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
 QY 61 MECAVNTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELEGEI 120  
 DB 61 MECAVNTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELEGEI 120

QY 121 TTNHKLQDASAEVERLERRENOVLSVRIDAKKYPPSSODSSAAAPOLLIVL 172  
 DB 121 TTNHKLQDASAEVERLERRENOVLSVRIDAKKYPPSSODSSAAAPOLLIVL 172

RESULT 3  
 ID AAM62207 standard; protein; 180 AA.  
 AC AAM62207;  
 DT 21-SEP-1998 (first entry)

DE Humanised anti-HML.24 antibody polypeptide.

XX Mouse; human; humanised; anti-HML.24 antibody; myeloma; FR; CDR;  
 KM framework region; complementarity determining region; antigenicity.

OS Synthetic.

OS Mus sp.

OS Homo sapiens.

PD 09-APR-1998.

PF 03-OCT-1997; 97WO-JP003553.

PR 04-OCT-1996; 96JP-00264756.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Ono K, Ohtomo T, Tsuchiya M, Yoshimura Y, Kohshihara Y, Kosaka M;  
 DR MPI: 1998-286421/25.

DR N-PSDB; AAV39359.

PT Humanised anti-HML.24 antibody - for treatment of myeloma.

PS Claim 81; Page 151-153; 210pp; Japanese.

XX A humanised anti-HML.24 antibody has been developed which comprises human  
 CC L and H chain C regions, and L and/or H chain V regions containing  
 CC material originating in mouse anti-HML.24 antibody. The V regions contain  
 CC framework (FR) regions of human origin and complementarity determining  
 CC regions (CDR) of mouse origin, leading to a reshaped humanised antibody.  
 CC The C regions are human Ck (L-chain) and human C gamma (especially C  
 CC gamma 1) (H-chain). The FR regions of the L chain V region are derived  
 CC from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions  
 CC of the H chain V region are derived from human subtype HSG1 (e.g. FR1-3  
 CC from human antibody Hg3 and FR4 from human antibody Hg6). The present  
 CC sequence represents an antibody polypeptide from the present invention.  
 CC The antibodies are used for the treatment of myeloma, especially by  
 CC injection, intravenously, intramuscularly or subcutaneously. The  
 CC antibodies are used at 0.01-1000 (especially 5-100) mg/kg body weight.  
 CC The humanised antibody has low antigenicity and is therefore effective  
 CC therapeutically in humans

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
 QY 61 MECAVNTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELEGEI 120  
 DB 61 MECAVNTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELEGEI 120

OY 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172  
 DB 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172

RESULT 4  
 ID AAY02576  
 AAY02576 standard; protein; 180 AA.

AC AAY02576;  
 AC AAY02576;  
 DT 16-JUL-1999 (first entry)  
 DE HMI.24 antigenic protein.  
 DE HMI.24 antigenic protein.  
 KW Reconstituted human antibody; peptide antigen HMI.24; framework region; complementary determining region; CDR; anti-HMI.24 antibody; myeloma; humanised antibody.  
 KW humanised antibody.  
 OS Homo sapiens.  
 OS Homo sapiens.  
 PN WO9918212-A1.  
 PD 15-APR-1999.  
 PD 15-APR-1999.  
 PF 02-OCT-1998; 98WO-JP004469.  
 PF 02-OCT-1998; 98WO-JP004469.  
 PR 03-OCT-1997; 97JP-00271726.  
 PR 03-OCT-1997; 97JP-00271726.

PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PI Tsuchiya M;  
 PI Tsuchiya M;  
 DR WPI; 1999-277273/23.  
 DR WPI; 1999-277273/23.  
 DR N-PSDB; AAX59485.  
 DR N-PSDB; AAX59485.  
 PT Reconstituted human antibody useful in the treatment of myeloma.  
 PT Reconstituted human antibody useful in the treatment of myeloma.  
 PS Disclosure; Page 131-133; 256pp; Japanese.  
 PS Disclosure; Page 131-133; 256pp; Japanese.  
 XX The specification describes a reconstituted human antibody recognising  
 XX The specification describes a reconstituted human antibody recognising  
 XX the peptide antigen HMI.24. This human antibody contains natural human  
 XX the peptide antigen HMI.24. This human antibody contains natural human  
 XX framework regions modified by amino acid substitutions to provide  
 XX framework regions modified by amino acid substitutions to provide  
 XX homogeneity with a previously designed framework region (which may arise  
 XX homogeneity with a previously designed framework region (which may arise  
 XX from a human or non-human source); and complementary determining regions  
 XX from a human or non-human source); and complementary determining regions  
 XX (CDR) derived from a non-human anti-HMI.24 antibody. The reconstituted  
 XX (CDR) derived from a non-human anti-HMI.24 antibody. The reconstituted  
 XX antibody is useful in the treatment of diseases in which the surface  
 XX antibody is useful in the treatment of diseases in which the surface  
 XX antigen HMI.24 is implicated such as myeloma. The present sequence  
 XX antigen HMI.24 is implicated such as myeloma. The present sequence  
 XX represents HMI.24 antigenic protein  
 XX represents HMI.24 antigenic protein  
 SO Sequence 180 AA;  
 SO Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIIFITIKANSEACRDLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIIFITIKANSEACRDLRAV 60  
 OY 61 MECAVTHLLOELTEAOKGFQDVEAQAATCNHTVMALMASIDAEKAOQKVEELGEI 120  
 DB 61 MECAVTHLLOELTEAOKGFQDVEAQAATCNHTVMALMASIDAEKAOQKVEELGEI 120  
 OY 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172  
 DB 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172

RESULT 5  
 ID AAY32765  
 AAY32765 standard; protein; 180 AA.

AC AAY32765;  
 XX 25-OCT-1999 (first entry)  
 DT 25-OCT-1999 (first entry)  
 DE Soluble HMI.24 antigenic protein sequence.  
 DE Soluble HMI.24 antigenic protein sequence.  
 DE HMI.24; antigenic protein; antibody; immunoassay; diagnosis; cancer;  
 DE HMI.24; antigenic protein; antibody; immunoassay; diagnosis; cancer;  
 KW immune disorder; immunotherapy monitoring.  
 KW immune disorder; immunotherapy monitoring.  
 OS Homo sapiens.  
 OS Homo sapiens.  
 PN WO9943703-A1.  
 PN WO9943703-A1.  
 PD 02-SEP-1999.  
 PD 02-SEP-1999.  
 PF 25-FEB-1999; 99WO-JP000885.  
 PF 25-FEB-1999; 99WO-JP000885.  
 PR 25-FEB-1998; 98JP-00060613.  
 PR 25-FEB-1998; 98JP-00060613.

PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PI Ozaki Y, Koishihara Y;  
 PI Ozaki Y, Koishihara Y;  
 DR WPI; 1999-51836/43.  
 DR WPI; 1999-51836/43.  
 DR N-PSDB; AAZ10917.  
 DR N-PSDB; AAZ10917.  
 PT Immunoassay of anti-HMI.24 antibody or soluble HMI.24 antigen, useful for  
 PT Immunoassay of anti-HMI.24 antibody or soluble HMI.24 antigen, useful for  
 PT diagnosis of immune disorders and cancer.  
 PT diagnosis of immune disorders and cancer.  
 PS Example 3; Fig 14-15; 138pp; Japanese.  
 PS Example 3; Fig 14-15; 138pp; Japanese.  
 XX This sequence represents a human soluble HMI.24 antigenic protein. The  
 XX This sequence represents a human soluble HMI.24 antigenic protein. The  
 XX invention relates to an immunochemical assay of anti-HMI.24 antibody by  
 XX invention relates to an immunochemical assay of anti-HMI.24 antibody by  
 XX use of a soluble HMI.24 antigenic protein, or an immunochemical assay of  
 XX use of a soluble HMI.24 antigenic protein, or an immunochemical assay of  
 XX the soluble antigen by use of the antibody. The immunoassay of the HMI.24  
 XX the soluble antigen by use of the antibody. The immunoassay of the HMI.24  
 XX antigen or antibody is useful for diagnosis of immune disorders and  
 XX antigen or antibody is useful for diagnosis of immune disorders and  
 XX cancer, for monitoring of anti-HMI.24 antibody immunotherapy, and for  
 XX cancer, for monitoring of anti-HMI.24 antibody immunotherapy, and for  
 XX assay of the antibody or antigen for investigative purposes, in  
 XX assay of the antibody or antigen for investigative purposes, in  
 XX biological samples such as blood, serum, urine, milk, synovial fluid or  
 XX biological samples such as blood, serum, urine, milk, synovial fluid or  
 XX microorganism culture media. The method is sensitive down to 500 pg/ml  
 XX microorganism culture media. The method is sensitive down to 500 pg/ml  
 XX antibody  
 XX antibody  
 SO Sequence 180 AA;  
 SO Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIIFITIKANSEACRDLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIIFITIKANSEACRDLRAV 60  
 OY 61 MECAVTHLLOELTEAOKGFQDVEAQAATCNHTVMALMASIDAEKAOQKVEELGEI 120  
 DB 61 MECAVTHLLOELTEAOKGFQDVEAQAATCNHTVMALMASIDAEKAOQKVEELGEI 120  
 OY 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172  
 DB 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172

RESULT 6  
 ID AAY33202  
 AAY33202 standard; protein; 180 AA.  
 AC AAY33202;  
 AC AAY33202;  
 DT 22-NOV-1999 (first entry)  
 DT 22-NOV-1999 (first entry)  
 DE Human HMI.24 antigenic protein.  
 DE Human HMI.24 antigenic protein.  
 KW Antigenic protein; HMI.24; splice variant; promoter; antineumatic;  
 KW Antigenic protein; HMI.24; splice variant; promoter; antineumatic;  
 KW antiarthritic; bone marrow; tumour cell; drug development; treatment;  
 KW antiarthritic; bone marrow; tumour cell; drug development; treatment;

KW myeloma, rheumatoid arthritis; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9943803-A1.  
 XX  
 PD 02-SEP-1999.  
 XX  
 PF 25-FEB-1999; 99WO-JP000884.  
 XX  
 PR 25-FEB-1999; 98JP-00060617.  
 XX  
 PR 24-MAR-1998; 98JP-00093883.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Ohtomo T, Tsuchiya M, Koishihara Y, Kosaka M;  
 XX  
 DR WPI, 1999-550869/46.  
 XX  
 DR N-PSDB; AAZ09726.  
 XX  
 PT Genomic DNA encoding Hm1.24 antigen protein as well as splicing variants,  
 XX  
 PT useful e.g. in development of drugs for treating myeloma and rheumatoid  
 XX  
 PT arthritis.  
 XX  
 PS Example 1; Fig 1-2; 83pp; Japanese.  
 XX  
 CC This invention describes a novel human antigenic protein, Hm1.24, its  
 XX  
 CC encoding nucleic acid, splice variants and promoter region. The products  
 XX  
 CC of the invention have antirheumatic and antiarthritic activity. The DNA  
 XX  
 CC of the invention is isolated from bone marrow tumour cells, which can be  
 XX  
 CC used to study the expression of Hm1.24 antigen, promoter activity of its  
 XX  
 CC promoter region, and in development of drugs in treating e.g. myeloma and  
 XX  
 CC rheumatoid arthritis. This sequence represents the human Hm1.24 antigenic  
 XX  
 CC protein described in the invention  
 XX  
 SQ Sequence 180 AA;  
 XX  
 Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASTSYDYCVRMEDGDRCKLLGIGLIVLIIIVLGVPLIIFITKANSEACRDLRAV 60  
 DB 1 MASTSYDYCVRMEDGDRCKLLGIGLIVLIIIVLGVPLIIFITKANSEACRDLRAV 60  
 QY 61 MECRNVTHTLQOELTEAOKGFQDVEAQAATCNHTVMALMASLDAEKAQOGKKVELEGRI 120  
 DB 61 MECRNVTHTLQOELTEAOKGFQDVEAQAATCNHTVMALMASLDAEKAQOGKKVELEGRI 120  
 QY 121 TTLNHLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSAAAPQLLIIVL 172  
 DB 121 TTLNHLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSAAAPQLLIIVL 172  
 RESULT 7  
 AAY05484  
 ID AAY05484 standard; protein; 180 AA.  
 XX  
 AC AAY05484;  
 XX  
 DT 07-JUL-1999 (first entry)  
 XX  
 DE Potentiator for antibody against lymphoid tumour.  
 XX  
 KW Antibody potentiator; lymphoid tumour; lymphoma; cytotoxic antibody;  
 XX  
 KW multiple myeloma; acute B-lymphocytoma; chronic B-lymphocytoma;  
 XX  
 KW pre-B-lymphoma; Burkitt's lymphoma; acute T-lymphocytoma; therapy;  
 XX  
 KW chronic T-lymphocytoma; PNTL.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9918997-A1.

PD 22-APR-1999.  
 XX  
 PF 14-OCT-1998; 98WO-JP004645.  
 XX  
 PR 14-OCT-1997; 97JP-00280759.  
 XX  
 PR 05-AUG-1998; 98JP-00222024.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Kosaka M, Koishihara Y;  
 XX  
 DR WPI, 1999-277447/23.  
 XX  
 DR N-PSDB; AAX36561.  
 XX  
 PT Potentiation of antibody treatment of lymphoma with biological response  
 XX  
 PT modifier.  
 XX  
 PS Claim 1; Page 37-38; 62pp; Japanese.  
 XX  
 CC This sequence represents a potentiator for an antibody against lymphoid  
 XX  
 CC tumour. The invention relates to a method for the treatment of lymphoma,  
 XX  
 CC in which a cytotoxic antibody is potentiated by administration of a  
 XX  
 CC biological response modifier. The method can be used for treatment of  
 XX  
 CC lymphomas and multiple myelomas which are resistant to conventional  
 XX  
 CC treatment, such as acute B-lymphocytoma, chronic B-lymphocytoma, pre-B  
 XX  
 CC lymphoma, Burkitt's lymphoma, acute T-lymphocytoma, chronic T-  
 XX  
 CC lymphocytoma, and PNTL  
 XX  
 SQ Sequence 180 AA;  
 XX  
 Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASTSYDYCVRMEDGDRCKLLGIGLIVLIIIVLGVPLIIFITKANSEACRDLRAV 60  
 DB 1 MASTSYDYCVRMEDGDRCKLLGIGLIVLIIIVLGVPLIIFITKANSEACRDLRAV 60  
 QY 61 MECRNVTHTLQOELTEAOKGFQDVEAQAATCNHTVMALMASLDAEKAQOGKKVELEGRI 120  
 DB 61 MECRNVTHTLQOELTEAOKGFQDVEAQAATCNHTVMALMASLDAEKAQOGKKVELEGRI 120  
 QY 121 TTLNHLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSAAAPQLLIIVL 172  
 DB 121 TTLNHLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSAAAPQLLIIVL 172  
 RESULT 8  
 AAY07250  
 ID AAY07250 standard; protein; 180 AA.  
 XX  
 AC AAY07250;  
 XX  
 DT 06-JUL-1999 (first entry)  
 XX  
 DE BST-2 protein.  
 XX  
 KW Mouse; BST-2; monoclonal antibody; R838; myeloma; cytotoxic activity.  
 XX  
 KW Mus sp.  
 XX  
 PN JP11092399-A.  
 XX  
 PD 06-APR-1999.  
 XX  
 PF 24-SEP-1997; 97JP-00274960.  
 XX  
 PR 24-SEP-1997; 97JP-00274960.  
 XX  
 PA (CHUS ) CHUGAI PHARM CO LTD.  
 XX  
 DR WPI, 1999-283503/24.  
 XX  
 DR N-PSDB; AAX29996.

XX An agent for treating myeloma -includes an antibody and has cytotoxic  
 PT activity.  
 XX

PS Claim 1; Page 10; 13pp; Japanese.

CC This sequence represents the mouse BSR-2 protein which is used to raise  
 CC antibodies, especially the monoclonal antibody RS38. The antibody can be  
 CC used in compositions to treat myelomas when the antibody is associated  
 CC with a cytotoxic activity  
 XX

SQ Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPILITIKANSEACRDGLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPILITIKANSEACRDGLRAV 60  
 QY 61 MECRVVTHLLOELTEAKGFQDVDAQAATCNHTVMALMASIDAEKAGOKKVEELGEI 120  
 DB 61 MECRVVTHLLOELTEAKGFQDVDAQAATCNHTVMALMASIDAEKAGOKKVEELGEI 120  
 QY 121 TILNHKLDASAEVERLRRENQVLSVRIADKKYIPSSODSSAAAPOLLIVL 172  
 DB 121 TILNHKLDASAEVERLRRENQVLSVRIADKKYIPSSODSSAAAPOLLIVL 172

RESULT 9

AA53273  
 ID AAY53273 standard; protein; 180 AA.

XX AAY53273;

AC 21-JUN-2000 (first entry)

DE Human Hm1.24 antigen protein sequence SEQ ID NO:2.

XX Human; Hm1.24 antigen protein; detection; plasmocytoma; multiple myeloma;  
 KW plasmocytic leukemia; extramedullary plasmocytoma;  
 KW multiple plasmocytoma; asymptomatic myeloma.

XX Homo sapiens.

OS WO200017395-A1.

PN 30-MAR-2000.

PD 20-AUG-1999; 99WO-JP004502.

PF 18-SEP-1998; 98JP-00264593.

PR (CHUS) CHUGAI SEIYAKU KK.

PA Kawai S, Koshihara Y, Kosaka M;

PI WPI; 2000-283616/24.

DR N-PSDB; AAA13654.

PT Detection of measurement of plasmocytomas, applicable for early diagnosis  
 PT of e.g. multiple myeloma and plasmocytic leukemia, using a polynucleotide  
 PT which is expressed specifically or strongly in plasmocytomas.

PS Disclosure; Page 15-16; 20pp; Japanese.

XX A method has been developed for detecting or measuring plasmocytomas in a  
 CC sample at an early stage of disease development. The method comprises  
 CC amplifying a polynucleotide which is expressed specifically or strongly  
 CC in plasmocytomas before quantifying the amplification product by  
 CC comparing with results obtained with a control sample. The method is for  
 CC detecting or measuring plasmocytomas, applicable for early diagnosis of

CC e.g. multiple myeloma, plasmocytic leukemia, isolated plasmocytoma,  
 CC extramedullary plasmocytoma, multiple plasmocytoma obtained from smoking  
 CC or asymptomatic myeloma. The present sequence represents human Hm1.24  
 CC antigen protein, which is expressed in plasmocytomas and so can be used  
 CC in the method of the invention  
 XX

SQ Sequence 180 AA;

Query Match 100.0%; Score 854; DB 3; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPILITIKANSEACRDGLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPILITIKANSEACRDGLRAV 60  
 QY 61 MECRVVTHLLOELTEAKGFQDVDAQAATCNHTVMALMASIDAEKAGOKKVEELGEI 120  
 DB 61 MECRVVTHLLOELTEAKGFQDVDAQAATCNHTVMALMASIDAEKAGOKKVEELGEI 120  
 QY 121 TILNHKLDASAEVERLRRENQVLSVRIADKKYIPSSODSSAAAPOLLIVL 172  
 DB 121 TILNHKLDASAEVERLRRENQVLSVRIADKKYIPSSODSSAAAPOLLIVL 172

RESULT 10

AAB70697  
 ID AAB70697 standard; protein; 180 AA.

XX AAB70697;

AC 18-MAY-2001 (first entry)

DE Human Hm1.24 antigen protein sequence SEQ ID NO:2.

XX Human; Hm1.24 antigen expression potentiator; Hm1.24 protein antigen;  
 KW myeloma; interferon alpha; interferon gamma; IFN-alpha; IFN-gamma;  
 KW interferon regulatory factor 2; IRF-2; cytostatic; cytotoxic antibody;  
 KW multiple myeloma.

OS Homo sapiens.

PN WO200113940-A1.

PD 01-MAR-2001.

PF 22-AUG-2000; 2000WO-JP005617.

PR 23-AUG-1999; 99JP-00236007.

PR 16-FEB-2000; 2000JP-00038689.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Kosaka M, Ozaki S, Wakahara Y;

DR WPI; 2001-202921/20.

DR N-PSDB; AAF74792.

PT Hm1.24 antigen expression potentiating agent containing interferon alpha  
 PT or gamma or IRF-2 for treatment of myeloma.

PS Claim 1; Page 55-56; 72pp; Japanese.

XX The present invention describes an agent for potentiating the expression  
 CC of Hm1.24 antigen in myeloma cells. The agent contains as an active  
 CC component interferon (IFN) alpha or gamma, or interferon regulatory  
 CC factor 2 (IRF-2), or a compound promoting the expression of IRF-2. Also  
 CC described are: (1) drug compositions for the treatment of myeloma which  
 CC contain the Hm1.24 antigen expression potentiating agent together with a  
 CC cytotoxic antibody binding to Hm1.24 antigen; (2) screening compounds for  
 CC their activity in potentiating the expression of IRF-2; and (3) kits for  
 CC the treatment of myeloma using the Hm1.24 antigen expression potentiating  
 CC agent and a cytotoxic antibody. The agent has cytostatic activity and can

CC be used for the treatment of myeloma, especially of multiple myeloma. The  
 CC present sequence represents the human Hm1.24 protein antigen

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 4; Length 180;

Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIFITIKNSACRCDGLRAV 60

DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIFITIKNSACRCDGLRAV 60

QY 61 MECRNVTHTLLOELTEAKGQFQDVEAQAATCNHTVMALMSLDKAKQGGKVEELGEI 120

DB 61 MECRNVTHTLLOELTEAKGQFQDVEAQAATCNHTVMALMSLDKAKQGGKVEELGEI 120

QY 121 TITNHLKQDASAEVRLRRENOVLSVRIADKKYPPSSODSSAAPOLLIVL 172

DB 121 TITNHLKQDASAEVRLRRENOVLSVRIADKKYPPSSODSSAAPOLLIVL 172

RESULT 11

ABBS0295

ID ABB50295 standard; protein; 180 AA.

AC ABB50295;

XX 08-FEB-2002 (first entry)

DE Bone marrow stromal antigen (BST-2) ovarian tumour marker protein, #80.

XX Ovarian tumour marker gene; human; overexpression; upregulation;

XX epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;

KM identification; serous cystadenoma; borderline serous tumour;

KM serous cystadenocarcinoma; mucinous cystadenocarcinoma;

KM mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;

KM undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;

KM adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;

KM immune response pathway; cell proliferation regulation; protein folding;

KM membrane localised; secreted; therapeutic target; cytostatic;

XX gene therapy; vaccine.

OS Homo sapiens.

XX WO200175177-A2.

XX 03-APR-2001; 2001WO-US010947.

XX 03-APR-2000; 2000US-0194336P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;

XX WPI; 2001-626450/72.

XX N-PSDB; ABA83121.

XX Detecting and identifying ovarian tumor, identifying increased risk for

XX developing ovarian cancer, and determining effectiveness of ovarian

XX cancer treatment, by measuring expression level of ovarian tumor marker

XX gene.

CC at increased risk for developing ovarian cancer, in prognostic tests for

CC assessing the relative severity of ovarian cancer, in tests for

CC monitoring a patient in remission from ovarian cancer and in tests for

CC monitoring disease status in a patient being treated for ovarian cancer.

CC The methods can additionally be used to identify a particular tumour as

CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from

CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,

CC mucinous cystadenoma, endometrioid carcinoma, undifferentiated carcinoma,

CC cystadenocarcinoma, cystadenofibroma, adenofibroma and Brenner

CC tumour. The ovarian tumour marker genes of the invention were identified

CC using SAGE (serial analysis of gene expression) and were found to be

CC overexpressed in a broad variety of ovarian epithelial tumour cells

CC relative to normal ovarian epithelial cells. The marker genes are

CC implicated in immune response pathways, in the regulation of cell

CC proliferation and in protein folding, and many of these are membrane-

CC localised or secreted. In addition to their use as diagnostic and

CC prognostic markers, the ovarian tumour marker genes or their encoded

CC proteins may be used as therapeutic targets for the treatment and

CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent

CC proteins encoded by ovarian tumour marker genes of the invention

XX Sequence 180 AA;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIFITIKNSACRCDGLRAV 60

DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIFITIKNSACRCDGLRAV 60

QY 61 MECRNVTHTLLOELTEAKGQFQDVEAQAATCNHTVMALMSLDKAKQGGKVEELGEI 120

DB 61 MECRNVTHTLLOELTEAKGQFQDVEAQAATCNHTVMALMSLDKAKQGGKVEELGEI 120

QY 121 TITNHLKQDASAEVRLRRENOVLSVRIADKKYPPSSODSSAAPOLLIVL 172

DB 121 TITNHLKQDASAEVRLRRENOVLSVRIADKKYPPSSODSSAAPOLLIVL 172

RESULT 12

ABBS3492

ID ABB83492 standard; protein; 180 AA.

AC ABB83492;

XX 04-OCT-2002 (first entry)

DE Human Bone Marrow Stromal Antigen 2, BST2.

XX Human; bone marrow stromal antigen 2; BST2; cytostatic; antirheumatic;

XX antigen; lymphoma; cancer; multiple myeloma; rheumatism.

XX Homo sapiens.

XX WO200257316-A1.

XX 25-JUL-2002.

XX 26-DEC-2001; 2001WO-JP011493.

XX 28-DEC-2000; 2000JP-00403245.

XX (KIRI ) KIRIN BEER KK.

XX Tahara T,

XX WPI; 2002-557847/59.

XX N-PSDB; ABB8330.

XX Monoclonal antibody binding to human cell surface antigen BST2 for

XX treatment and diagnosis of cancer rheumatism and lymphoma.

XX Claim 7; Fig 5; 49pp; Japanese.

PS The present invention relates to a monoclonal antibody, which can bind to  
XX human cell surface antigen Bst2 (Bone Marrow Stromal Antigen 2), and is  
CC capable of internalizing into the cell. A complex, comprising the  
CC monoclonal antibody and a therapeutic drug, can be used for treatment of  
CC lymphoma, cancer, multiple myeloma and rheumatism. The antibody complex  
CC effectively introduces the bound drug to the cell interior. The present  
CC sequence is the protein sequence for human Bst2

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 5; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDRCVPMEDGDKRCKLLIGILVLLIIVILGVPILITITKANSEACRDLRAV 60  
DB 1 MASTSYDRCVPMEDGDKRCKLLIGILVLLIIVILGVPILITITKANSEACRDLRAV 60  
QY 61 MECRNVTHTLQOELTEAQKGFQDVEAQAATCNHTWALMASIDAEKAGQCKVELEGEI 120  
DB 61 MECRNVTHTLQOELTEAQKGFQDVEAQAATCNHTWALMASIDAEKAGQCKVELEGEI 120  
QY 121 TTLNKHLDQASAEVERLRRENOVLSVRIADKKYPSODSSAAAPQLLIVL 172  
DB 121 TTLNKHLDQASAEVERLRRENOVLSVRIADKKYPSODSSAAAPQLLIVL 172

#### RESULT 13

ABP53548 ID ABP53548 standard; protein; 180 AA.

XX ABP53548;

DT 14-DEC-2002 (first entry)

XX Human HML.24 protein antigen SEQ ID NO:2.

XX Human; HML.24 protein antigen; tumour; hematopoietic; interferon alpha;  
KW Interferon gamma; IRF-2; interferon-regulatory factor-2; cytostatic;  
KM Leukaemia; lymphoma; myeloma.

XX Homo sapiens.

OS WO200264159-A1.

XX 22-AUG-2002.

XX 06-FEB-2002; 2002WO-JP000989.

XX 07-FEB-2001; 2001JP-00031492.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Kosaka M, Ozaki S, Wakahara Y;

XX WPI: 2002-682719/73.

DR N-PSDB; ABQ82202.

PT Remedies for tumors in hematopoietic organs e.g. leukemia, lymphoma or  
PT myeloma, containing HML.24 antigen expression inducers or potentiators in  
PT tumor cells e.g. interferon approximately or approximately, or IRF-2  
PT and anti-HML.24 antibody.

XX Claim 1; Page 73; 93pp; Japanese.

XX The present invention describes expression potentiators (I) or inducers  
CC of the human HML.24 protein antigen 180 amino acid residue sequence (II)  
CC in tumour cells of hematopoietic organs containing interferon alpha or  
CC gamma or IRF-2 (interferon-regulatory factor-2) protein as an active  
CC ingredient. Also described are remedies or drug compositions for tumours

CC in hematopoietic organs containing interferon alpha or gamma or IRF-2  
CC protein, and an antibody binding specifically to HML.24, or their various  
CC combinations. (I) have cytostatic activities. The remedies can be used  
CC for treating tumors in hematopoietic organs e.g. leukemia, lymphoma or  
CC myeloma. The present sequence represents the human HML.24 protein antigen  
CC from the present invention

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 5; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDRCVPMEDGDKRCKLLIGILVLLIIVILGVPILITITKANSEACRDLRAV 60  
DB 1 MASTSYDRCVPMEDGDKRCKLLIGILVLLIIVILGVPILITITKANSEACRDLRAV 60  
QY 61 MECRNVTHTLQOELTEAQKGFQDVEAQAATCNHTWALMASIDAEKAGQCKVELEGEI 120  
DB 61 MECRNVTHTLQOELTEAQKGFQDVEAQAATCNHTWALMASIDAEKAGQCKVELEGEI 120  
QY 121 TTLNKHLDQASAEVERLRRENOVLSVRIADKKYPSODSSAAAPQLLIVL 172  
DB 121 TTLNKHLDQASAEVERLRRENOVLSVRIADKKYPSODSSAAAPQLLIVL 172

#### RESULT 14

ABP61469 ID ABP61469 standard; protein; 180 AA.

XX ABP61469;

DT 30-SEP-2002 (first entry)

XX Human NF-kB activating protein SEQ ID NO 91.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;  
KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;  
KM neuroprotective; anti-HIV; autoimmune disease; cancer; infection;  
KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX Homo sapiens.

OS WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP011389.

XX 28-DEC-2000; 2000JP-00402288.

XX 26-MAR-2001; 2001JP-00088912.

XX 24-AUG-2001; 2001JP-00254018.

XX (ASAH) ASAH KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI: 2002-583617/62.

DR N-PSDB; ABQ91957.

PT NF-approximatelykB activating gene and expressed protein, applicable in  
PT diagnosis and screening inhibitors or promoters to control excessive  
PT activation or inhibition for treating e.g. inflammations, autoimmune  
PT diseases and cancer.

XX Claim 1; Page 413-414; 841pp; Japanese.

XX The invention relates to a purified protein (I), comprising one of 90  
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
CC the sequences but with some amino acids deleted, substituted or added and  
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and  
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
CC inhibitors or promoters to control excessive activation or inhibition and

CC for treating e.g. inflammations, autoimmune diseases, cancers,  
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
CC disorders  
XX  
SQ Sequence 180 AA;

Query Match. 100.0%; Score 854; DB 5; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASTSYDYCRVPMEDGDKCKLLIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV 60  
DB 1 MASTSYDYCRVPMEDGDKCKLLIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV 60  
OY 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASIDAEKAOQKKVEELBGEI 120  
DB 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASIDAEKAOQKKVEELBGEI 120  
OY 121 TTLNHLQDASAEVERLRRENOVLSYRIADKYYPSQDSSSAAAPOLLIVL 172  
DB 121 TTLNHLQDASAEVERLRRENOVLSYRIADKYYPSQDSSSAAAPOLLIVL 172

RESULT 15

AA52356  
ID AAM52356 standard; protein; 180 AA.

AC AAM52356;

DT 25-JAN-2002 (first entry)

DE Human Hm1.24 antigen which is expressed on cell membranes.

KW Hm1.24 antigen; antibody; extracellular domain; immunoassay; human.

OS Homo sapiens.

PN WO200177362-A1.

PD 18-OCT-2001.

PF 05-APR-2001; 2001WO-JP002964.

PR 06-APR-2000; 2000JP-00105423.

PA (CHUS ) CHUGAI SEIYAKU KK.

PI Kinoshita Y, Iehikawa Y;

DR WPI; 2002-010919/01.

DR N-PSDB; ABA01226.

PT Preparation of soluble Hm1.24 antigen extracellular domain, useful for

PS immunoassay of Hm1.24 antigen.

PS Disclosure; Fig 6; 96pp; Japanese.

CC The present invention relates to a method for preparing soluble Hm1.24

CC antigen extracellular domain. The method comprises culturing animal cells

CC transformed by an expression vector carrying Erialpha (undefined).

CC promoter and Hm1.24 antigen gene. The invention can be used for

CC immunoassay of Hm1.24 antigen. The method is more sensitive to

CC conventional enzyme linked immunoassay (ELISA) methods. The

CC present sequence was used to illustrate the present invention

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 5; Length 180;

Best Local Similarity 100.0%; Pred. No. 6.9e-75;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASTSYDYCRVPMEDGDKCKLLIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV 60

DB 1 MASTSYDYCRVPMEDGDKCKLLIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV 60  
OY 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASIDAEKAOQKKVEELBGEI 120  
DB 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASIDAEKAOQKKVEELBGEI 120  
OY 121 TTLNHLQDASAEVERLRRENOVLSYRIADKYYPSQDSSSAAAPOLLIVL 172  
DB 121 TTLNHLQDASAEVERLRRENOVLSYRIADKYYPSQDSSSAAAPOLLIVL 172

Search completed: December 29, 2004, 11:45:39  
Job time : 84 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 11:11:07 / Search time 27 Seconds  
(without alignments)  
422.470 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854

Sequence: 1 MASTSYDCRVPMDGDKRC.....TYPSSQSSSAAPQLIVL 172

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854	100.0	180	2	US-08-624-650-1
2	854	100.0	180	4	US-09-818-648-1
3	854	100.0	180	4	US-09-355-925-5
4	854	100.0	180	4	US-09-787-375-2
5	854	100.0	180	4	US-09-622-166A-3
6	854	100.0	180	4	US-09-263-921-129
7	490	57.4	156	4	US-09-622-166A-20
8	99.5	11.7	270	2	US-09-055-095-4
9	99.5	11.7	270	2	US-08-809-494A-2
10	99.5	11.7	270	3	US-09-352-302-2
11	99.5	11.7	273	2	US-08-809-494A-4
12	99.5	11.7	273	3	US-09-352-302-4
13	95.5	11.2	977	4	US-09-010-147B-18
14	95	11.1	885	2	US-08-533-306A-4
15	95	11.1	885	2	US-08-742-923A-4
16	95	11.1	1857	4	US-09-917-254-91
17	95	11.1	1937	4	US-09-538-092-918
18	95	11.1	1972	4	US-08-875-435B-4
19	95	11.1	1972	4	US-09-538-092-1084
20	93	10.9	210	4	US-08-875-435B-3
21	92.5	10.8	292	2	US-09-222-938A-67
22	92.5	10.8	292	2	US-08-688-342-4
23	92.5	10.8	292	2	US-09-113-788-4
24	92.5	10.8	292	2	US-09-862-802A-12
25	92.5	10.8	392	4	US-09-583-110-4374
26	92.5	10.8	534	4	US-09-103-664A-2
27	92.5	10.8	1886	3	US-08-938-105-3

28	92	10.8	165	4	US-09-898-554-24	Sequence 24, Appl
29	90.5	10.6	1935	4	US-09-538-092-916	Sequence 916, App
30	90.5	10.6	1939	4	US-09-538-092-915	Sequence 915, App
31	89.5	10.5	316	3	US-09-111-470-4	Sequence 4, Appl
32	89.5	10.5	316	4	US-09-862-802A-4	Sequence 20, Appl
33	89	10.4	363	4	US-09-898-554-20	Sequence 4, Appl
34	88.5	10.4	397	4	US-09-252-991A-23027	Sequence 23027, A
35	88.5	10.4	1939	3	US-09-310-187A-1	Sequence 1, Appl
36	88.5	10.4	1939	4	US-09-538-092-917	Sequence 917, App
37	88.5	10.4	1940	4	US-09-538-092-901	Sequence 901, App
38	88	10.3	207	4	US-09-898-554-26	Sequence 26, Appl
39	88	10.3	288	3	US-08-312-949-4	Sequence 4, Appl
40	88	10.3	288	3	US-08-446-201-4	Sequence 4, Appl
41	88	10.3	619	1	US-08-465-746-2	Sequence 2, Appl
42	88	10.3	619	1	US-08-214-164-2	Sequence 2, Appl
43	88	10.3	619	2	US-08-467-852A-3	Sequence 3, Appl
44	88	10.3	619	2	US-08-246-836-2	Sequence 2, Appl
45	88	10.3	619	2	US-08-247-491A-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-08-624-650-1  
Sequence 1, Application US/08624650  
Patent No. 5914252  
GENERAL INFORMATION:  
APPLICANT: HIRANO, TOSHIO  
APPLICANT: KAIISHO, TSUNEYASU  
TITLE OF INVENTION: MEMBERANE PROTEIN POLYPEPTIDE HAVING  
TITLE OF INVENTION: PER-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/624, 650  
FILING DATE: 22-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/01732  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-281622  
FILING DATE: 15-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 7625-001-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2230  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-624-650-1  
Query Match 100.0%; Score 854; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.4e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVMEDEGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Db 1 MASTSYDYCRVMEDEGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Qy 61 MCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGOKVEELGEI 120

Db 61 MCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGOKVEELGEI 120

Qy 121 TILNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSODSSAAPOLLIVL 172

Db 121 TILNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSODSSAAPOLLIVL 172

RESULT 2  
US-09-818-648-1

/ Sequence 1, Application US/09818648

/ Patent No. 6489126

/ GENERAL INFORMATION:

/ APPLICANT: HIRANO, TOSHIO

/ TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING

/ PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF

/ NUMBER OF SEQUENCES: 2

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

/ P.C.

/ STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

/ CITY: ARLINGTON

/ STATE: VA

/ COUNTRY: USA

/ ZIP: 22202

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/818,648

/ FILING DATE: 28-Mar-2001

/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/08/624,650

/ FILING DATE: 22-MAY-1996

/ APPLICATION NUMBER: PCT/JP94/01732

/ FILING DATE: 14-OCT-1994

/ APPLICATION NUMBER: JP 5-281622

/ FILING DATE: 15-OCT-1993

/ ATTORNEY/AGENT INFORMATION:

/ NAME: OBLON, NORMAN F.

/ REGISTRATION NUMBER: 24,618

/ REFERENCE/DOCKET NUMBER: 7625-001-0 PCT

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 703-413-3000

/ TELEFAX: 703-413-2220

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 180 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-818-648-1

Query Match

Best Local Similarity 100.0%; Pred. No. 2.4e-84;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVMEDEGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Db 1 MASTSYDYCRVMEDEGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Qy 61 MCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGOKVEELGEI 120

Db 61 MCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGOKVEELGEI 120

Qy 121 TILNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSODSSAAPOLLIVL 172

Db 121 TILNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSODSSAAPOLLIVL 172

RESULT 3

US-09-355-925-5

/ Sequence 5, Application US/09355925

/ Patent No. 6503510

/ GENERAL INFORMATION:

/ APPLICANT: KOISHIBARA, YASUO

/ APPLICANT: YOSHIMURA, YASUSHI

/ TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS

/ FILE REFERENCE: 053466/0255

/ CURRENT APPLICATION NUMBER: US/09/355,925

/ PRIOR FILING DATE: 1999-08-11

/ PRIOR APPLICATION NUMBER: PCT/JP98/00568

/ PRIOR FILING DATE: 1998-02-12

/ PRIOR APPLICATION NUMBER: JP 9-41410

/ PRIOR FILING DATE: 1997-02-12

/ NUMBER OF SEQ ID NOS: 8

/ SOFTWARE: Patentin Ver. 2.1

/ SEQ ID NO 5

/ LENGTH: 180

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE:

/ OTHER INFORMATION: Amino acid sequence of Hm1.24 antigen

US-09-355-925-5

Query Match

Best Local Similarity 100.0%; DB 4; Length 180;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVMEDEGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Db 1 MASTSYDYCRVMEDEGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Qy 61 MCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGOKVEELGEI 120

Db 61 MCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGOKVEELGEI 120

Qy 121 TILNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSODSSAAPOLLIVL 172

Db 121 TILNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSODSSAAPOLLIVL 172

RESULT 4

US-09-787-375-2

/ Sequence 2, Application US/09787375

/ Patent No. 6602663

/ GENERAL INFORMATION:

/ APPLICANT: KAMAI, SHIGETO

/ APPLICANT: KOISHIBARA, YASUO

/ TITLE OF INVENTION: METHOD FOR DETECTION OR MEASUREMENT OF PLASMACYTOMA CELLS

/ FILE REFERENCE: 053466/0301

/ CURRENT APPLICATION NUMBER: US/09/787,375

/ PRIOR FILING DATE: 2001-03-16

/ PRIOR APPLICATION NUMBER: PCT/JP99/04502

/ PRIOR FILING DATE: 1999-08-20

/ PRIOR APPLICATION NUMBER: JP 10-264593

/ NUMBER OF SEQ ID NOS: 5

/ SOFTWARE: Patentin Ver. 2.1

/ SEQ ID NO 2

/ LENGTH: 180

/ TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of HM1.24 antibody protein  
US-09-787-315-2

Query Match 100.0%; Score 854; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2.4e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MASTSYDVCYRVMEGDGRCCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
1 MASTSYDVCYRVMEGDGRCCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
Qy 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
Db 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
Qy 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172  
121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172  
Db 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172

RESULT 5  
US-09-622-166a-3  
Sequence 3, Application US/09622166a  
Patent No. 6613546  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
APPLICANT: KOISHIHARA, YASUO  
APPLICANT: KOSAKA, MASAOKI  
TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND  
TITLE OF INVENTION: PROMOTER THEREOF  
FILE REFERENCE: 053466/0285  
CURRENT APPLICATION NUMBER: US/09/622,166a  
CURRENT FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: PCT/JP99/00884  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: 10-60617  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 10-93883  
PRIOR FILING DATE: 1998-03-24  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-622-166a-3

Query Match 100.0%; Score 854; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2.4e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MASTSYDVCYRVMEGDGRCCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
1 MASTSYDVCYRVMEGDGRCCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
Qy 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
Db 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
Qy 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172  
121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172  
Db 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172

RESULT 6  
US-09-269-921-129  
Sequence 129, Application US/09269921  
Patent No. 6699974  
GENERAL INFORMATION:  
APPLICANT: Ono, Koichiro

APPLICANT: Ohtomo, Toshihiko  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yoshimura, Yasushi  
APPLICANT: Koishihara, Yasuo  
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
FILE REFERENCE: 35029-20007.00  
CURRENT APPLICATION NUMBER: US/09/269,921  
CURRENT FILING DATE: 1999-04-01  
EARLIER APPLICATION NUMBER: PCT/JP97/03553  
EARLIER FILING DATE: 1997-10-03  
EARLIER APPLICATION NUMBER: JP 8-264756  
EARLIER FILING DATE: 1996-10-04  
NUMBER OF SEQ ID NOS: 137  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 129  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
US-09-269-921-129

Query Match 100.0%; Score 854; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2.4e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MASTSYDVCYRVMEGDGRCCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
1 MASTSYDVCYRVMEGDGRCCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
Qy 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
Db 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAASLDAAKAGOKKVEELGEI 120  
Qy 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172  
121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172  
Db 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIYL 172

RESULT 7  
US-09-622-166a-20  
Sequence 20, Application US/09622166a  
Patent No. 6613546  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
APPLICANT: KOISHIHARA, YASUO  
APPLICANT: KOSAKA, MASAOKI  
TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND  
TITLE OF INVENTION: PROMOTER THEREOF  
FILE REFERENCE: 053466/0285  
CURRENT APPLICATION NUMBER: US/09/622,166a  
CURRENT FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: PCT/JP99/00884  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: 10-60617  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 10-93883  
PRIOR FILING DATE: 1998-03-24  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 20  
LENGTH: 156  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-622-166a-20

Query Match 57.4%; Score 490; DB 4; Length 156;  
Best Local Similarity 85.6%; Pred. No. 4e-45;  
Matches 101; Conservative 4; Mismatches 11; Indels 2; Gaps 2;  
Db 1 MASTSYDVCYRVMEGDGRCCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Db 1 MASTSDYCRVMEBQDKCKLLIGLIVLIIIVLIGVPLIIFITKANSEACRGLRAV 60  
QY 61 MECRNVTLLLOQLTEAOKGFQDVEAQAATCNHTMALASLDAEKAQOKVBELEG 118  
Db 61 MECRNVTLLLOQLTEAOKGFQDVEAQAATCNHTYAR-KPGIKREN-RQOEVLPLPG 116

## RESULT 8

US-09-055-095-4  
; Sequence 4, Application US/09055095  
; Patent No. 5945308  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Patterson, Chandra  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Sacher, Susan  
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/055,095  
; FILING DATE: Filed Herewith  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER:  
; ATTORNEY/AGENT INFORMATION:  
; FILING DATE:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0500 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 270 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1902982  
; US-09-055-095-4

Query Match 11.7%; Score 99.5; DB 2; Length 270;  
Best Local Similarity 25.9%; Pred. No. 0.013;  
Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGLIVLIIIVLIGVPLIIFITKANSEACRGLRAVMECRNVTLLLOQLTEAOKGFQ 82  
Db 40 VLCLGLVTVIILIIQLSQVSDLIKQ-----ANITH--QEDILEGQ----- 80  
QY 83 DVEAQAATCNHTMALASLDAEKAQOKVBELEGITTLNKKLQDASAEVERLRRENO 142  
Db 81 -----ILAQRRSEKS-AQESQKELKEMITFLAKDKDESKKLMELHRQNL 124  
QY 143 VLSVRIADKKY--PSSQD 159  
Db 125 NLQEVILKEAANYSGPCPD 143

RESULT 9  
US-08-809-494A-2  
; Sequence 2, Application US/08809494A  
; Patent No. 5962260  
; GENERAL INFORMATION:  
; APPLICANT: Sawamura, Tatsuya  
; APPLICANT: Masaki, Tomoo  
; TITLE OF INVENTION: Modified Low-Density Lipoprotein  
; TITLE OF INVENTION: Receptor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAlulay Fisher Nissen Goldberg & Kiel  
; STREET: 261 Madison Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,494A  
; FILING DATE: 24-MAR-1997  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-321705  
; FILING DATE: 30-NOV-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-214206  
; FILING DATE: 31-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldberg, Jules E  
; REGISTRATION NUMBER: 24408  
; REFERENCE/DOCKET NUMBER: JG-YI-4363PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 818-9479  
; TELEFAX: 212 818-4090  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 270 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-809-494A-2

Query Match 11.7%; Score 99.5; DB 2; Length 270;  
Best Local Similarity 25.9%; Pred. No. 0.013;  
Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGLIVLIIIVLIGVPLIIFITKANSEACRGLRAVMECRNVTLLLOQLTEAOKGFQ 82  
Db 40 VLCLGLVTVIILIIQLSQVSDLIKQ-----ANITH--QEDILEGQ----- 80  
QY 83 DVEAQAATCNHTMALASLDAEKAQOKVBELEGITTLNKKLQDASAEVERLRRENO 142  
Db 81 -----ILAQRRSEKS-AQESQKELKEMITFLAKDKDESKKLMELHRQNL 124  
QY 143 VLSVRIADKKY--PSSQD 159  
Db 125 NLQEVILKEAANYSGPCPD 143

RESULT 10  
US-09-352-302-2  
; Sequence 2, Application US/09352302  
; Patent No. 6197937  
; GENERAL INFORMATION:  
; APPLICANT: Sawamura, Tatsuya  
; APPLICANT: Masaki, Tomoo  
; TITLE OF INVENTION: Modified Low-Density Lipoprotein  
; TITLE OF INVENTION: Receptor



APPLICATION NUMBER: JP 6-321705  
FILING DATE: 30-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-214206  
FILING DATE: 31-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E  
REGISTRATION NUMBER: 24408  
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 986-4090  
TELEFAX: 212 818-9479  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 273 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-352-302-4

Query Match 11.7%; Score 99.5; DB 3; Length 273;  
Best Local Similarity 25.9%; Pred. No. 0.014;  
Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 ILGIGILVLLIIVIGVPLIIFITIRANSBACRGLRAVMECRNVTHLLQDELTEAQKGFQ 82  
DB 43 VLCLGLVTLVILLIQLSGVSLIKKQ-----ANITH--QEDILKQ----- 83  
QY 83 DVEAQAATCNHTVMAIAMSIDAEKAGQGVKELEGEITLTHKQDASAEVRLRRENO 142  
DB 84 -----ILAQRRSEKS-AQBSQELKEMITLAKHKLDESKKLMELHROVL 127  
QY 143 VLSVRIADKKY--PSSQD 159  
DB 128 NLQEVTKEMANTSGPCPD 146

RESULT 13  
US-09-010-147B-18  
Sequence 18, Application US/09010147B  
Patent No. 6653445  
GENERAL INFORMATION:  
APPLICANT: Nt et al.  
TITLE OF INVENTION: Human Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,147B  
FILING DATE: 12-NOV-6653445-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,205  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 60/034,204  
FILING DATE: 21-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PF353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 977 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-010-147B-18

Query Match 11.2%; Score 95.5; DB 4; Length 977;  
Best Local Similarity 26.4%; Pred. No. 0.22;  
Matches 24; Conservative 23; Mismatches 43; Indels 1; Gaps 1;

QY 55 DGLRAVMECRNVTHLLQDELTEAQKGFQDVEAQAATCNHTVMAIAMSIDAEKAGQGVKE 114  
DB 282 DAAVAKSLRLRLNEMAAEKAKAAGAEKVKQVAVRQSEITAVQARQASVREHVKEVQ 341  
QY 115 ELEGEITLTHKQDASAEVRLRRENOVL 144  
DB 342 QLOGKIFTLQEQLENGPMTQLARLQGENSIL 372

RESULT 14  
US-08-533-306A-4  
Sequence 4, Application US/08533306A  
Patent No. 5837457  
GENERAL INFORMATION:  
APPLICANT: Liu, Pu  
APPLICANT: Collins, Francis S.  
APPLICANT: Siciliano, Michael J.  
TITLE OF INVENTION: Markers for Detection of Chromosome 16  
TITLE OF INVENTION: Rearrangements  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Harness, Dickey & Pierce, P.L.C.  
STREET: P.O. Box 828  
CITY: Bloomfield Hills  
STATE: MI  
COUNTRY: USA  
ZIP: 48303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/533,306A  
FILING DATE: September 25, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Deann F.  
REGISTRATION NUMBER: 36683  
REFERENCE/DOCKET NUMBER: 2115-00869CCOB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 641-1600  
TELEFAX: (810) 641-0270  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 885 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-533-306A-4

Query Match 11.1%; Score 95; DB 2; Length 885;  
Best Local Similarity 24.5%; Pred. No. 0.21;  
Matches 27; Conservative 18; Mismatches 55; Indels 10; Gaps 1;

QY 53 CRDGLRAVMECRNVTHLLQDELTEAQKGFQDVEAQAATCNHTVMAIAMSID- 103  
DB 215 CSDGRARAELNDKVHKLQNEVESVTGMLNBAEGATRLADAVASLSSQLODPTQELLQEE 274

Oy 104 -AEKAGQOKVEELEGITTLNHLKQDASAEVERLRRENQVLSVRIADKK 152  
 Db 275 TRQKLNVTSTKLRQLEERNSLQDQDEMEAKONLEHISTINIQLSQSK 324

RESULT 15

US-08-742-923A-4  
 ; Sequence 4, Application US/08742923A  
 ; Patent No. 5869611  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Pu  
 ; APPLICANT: Collins, Francis S.  
 ; APPLICANT: Siciliano, Michael J.  
 ; APPLICANT: Claxton, David  
 ; TITLE OF INVENTION: Markers for Detection of Chromosome 16  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
 ; STREET: P.O. Box 828  
 ; CITY: Bloomfield Hills  
 ; STATE: MI  
 ; COUNTRY: USA  
 ; ZIP: 48303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/742,923A  
 ; FILING DATE: No. 5869611ember 1, 1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, Dean F.  
 ; REGISTRATION NUMBER: 36683  
 ; REFERENCE/DOCKET NUMBER: 2115-00869DVC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (810) 641-1600  
 ; TELEFAX: (810) 641-0270  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 885 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-742-923A-4

Query Match 11.1%; Score 95; DB 2; Length 885;  
 Best Local Similarity 24.5%; Pred. No. 0.21; Mismatches 55; Indels 10; Gaps 1;  
 Matches 27; Conservative 18; Mismatches 55; Indels 10; Gaps 1;  
 Oy 53 CRDGLRAVMEGRCNVTLHLOQELTEAOKGFQDVEAQAATCNHTVMALMSLD----- 103  
 Db 215 CSDEKRAARALNDKXKQNEVESVTGMLNEBEGKAIKAKDVASLSQLODQTOELQEE 274  
 Oy 104 -AEKAGQOKVEELEGITTLNHLKQDASAEVERLRRENQVLSVRIADKK 152  
 Db 275 TRQKLNVTSTKLRQLEERNSLQDQDEMEAKONLEHISTINIQLSQSK 324

Search completed: December 29, 2004, 11:44:10  
 Job time : 28 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 11:31:07 ; Search time 589 Seconds  
(without alignments)  
105.048 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854  
Sequence: 1 MASTSYDCRVPMEDGDKRC.....YTPSQDSSAAAPQLITVL 172

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: Published Applications\_AA:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854	100.0	180	9	US-09-828-217-1
2	854	100.0	180	9	US-09-760-723-5
3	854	100.0	180	9	US-09-355-925-5
4	854	100.0	180	9	US-09-818-648-1
5	854	100.0	180	10	US-09-269-921-129
6	854	100.0	180	10	US-09-509-098-129
7	854	100.0	180	13	US-10-114-893-46
8	854	100.0	180	14	US-10-171-311-20
9	854	100.0	180	14	US-10-315-125-5
10	854	100.0	180	14	US-10-218-253-129
11	854	100.0	180	14	US-10-024-2884-91
12	854	100.0	180	14	US-10-042-211A-91
13	854	100.0	180	14	US-10-428-085-5

14	854	100.0	180	14	US-10-423-007-3	Sequence 3, Appli
15	854	100.0	180	15	US-10-257-021-80	Sequence 80, Appli
16	854	100.0	180	15	US-10-617-217A-91	Sequence 91, Appli
17	854	100.0	180	16	US-10-474-714-2	Sequence 2, Appli
18	854	100.0	180	16	US-10-451-947A-2	Sequence 2, Appli
19	854	100.0	180	16	US-10-755-889-386	Sequence 386, App
20	854	100.0	180	17	US-10-024-298A-91	Sequence 91, Appli
21	854	100.0	180	17	US-10-473-127-815	Sequence 815, App
22	854	100.0	180	17	US-10-473-127-816	Sequence 816, App
23	854	100.0	180	17	US-10-473-127-818	Sequence 818, App
24	854	100.0	180	17	US-10-473-127-820	Sequence 820, App
25	854	100.0	180	17	US-10-473-127-821	Sequence 821, App
26	854	100.0	180	17	US-10-473-127-823	Sequence 823, App
27	854	100.0	180	17	US-10-473-127-824	Sequence 824, App
28	854	100.0	180	17	US-10-473-127-828	Sequence 828, App
29	854	100.0	180	17	US-10-473-127-831	Sequence 831, App
30	854	100.0	180	17	US-10-473-127-832	Sequence 832, App
31	854	100.0	180	17	US-10-473-127-833	Sequence 833, App
32	854	100.0	180	17	US-10-473-127-834	Sequence 834, App
33	854	100.0	180	17	US-10-370-715B-238	Sequence 238, App
34	854	100.0	193	14	US-10-106-698-4721	Sequence 4721, App
35	854	100.0	193	17	US-10-473-127-817	Sequence 817, App
36	847	99.2	180	17	US-10-473-127-822	Sequence 822, App
37	824.5	96.5	197	17	US-10-473-127-819	Sequence 819, App
38	614.5	72.0	143	17	US-10-473-127-825	Sequence 825, App
39	614	71.9	132	17	US-10-473-127-825	Sequence 825, App
40	614	71.9	161	17	US-10-473-127-829	Sequence 829, App
41	579	67.8	147	17	US-10-473-127-830	Sequence 830, App
42	574.5	67.3	126	17	US-10-473-127-827	Sequence 827, App
43	524	61.4	148	15	US-10-264-049-4164	Sequence 4164, App
44	490	57.4	156	14	US-10-423-007-20	Sequence 20, Appli
45	454	53.2	91	15	US-10-424-599-221303	Sequence 221303,

ALIGNMENTS

US-09-828-217-1  
Sequence 1, Appli  
Patent No. US20010051710A1  
GENERAL INFORMATION:  
APPLICANT: KIRANO, TOSHIO  
TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING  
PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/828,217  
FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/182,563  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/JP94/01732  
FILING DATE: 14-OCT-1994  
APPLICATION NUMBER: JP 5-281622  
FILING DATE: 15-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 7625-001-0 PCT  
TELECOMMUNICATION INFORMATION:  
TOLL FREE PHONE: 703-413-2000

FORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

SEQUENCE	DESCRIPTION:	SEQ ID NO: 1:
US-09-828-217-1		

Query Match	100.0%;	Score 854;	DB 9;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 2e-74;		
Matches 172;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	MASTSYDYGCVEMEDDEKXCKLLGIGLIVLLI	IYILGVPILIFIKANSACDGR	RAV	60
Db	1	MASTSYDCRVEMEDDKRCKLLGIGLIVLLI	IYILGVPILIFIKANSACDGR	RAV
				60
Qy	MEGRNTHLLQRLTEAKGFQDVERQAATCNHTMAL	MASLDDEKAGQCKVEELGEI		120
Db	61	MEGRNTHLLQRLTEAKGFQDVERQAATCNHTMAL	MASLDDEKAGQCKVEELGEI	120
Qy	TTLNHKLQDASAEVRLRENOVLSYRLADKKTYTSS	QDSSGAAPOLLIVL		172
Db	121	TTLNHKLQDASAEVRLRENOVLSYRLADKKTYTSS	QDSSGAAPOLLIVL	172
Qy	TTLNHKLQDASAEVRLRENOVLSYRLADKKTYTSS	QDSSGAAPOLLIVL		172
Db	121	TTLNHKLQDASAEVRLRENOVLSYRLADKKTYTSS	QDSSGAAPOLLIVL	172

```

RESULT 2
US-09-760-723-5
? Sequence 5, Application US/09760723
? Patent No. US20020034507a1
? GENERAL INFORMATION:
? APPLICANT: KOISHIHARA, YASUO
? TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
? FILE REFERENCE: 053466/0295
? CURRENT APPLICATION NUMBER: US/09/760,723
? CURRENT FILING DATE: 2001-05-29
? PRIOR APPLICATION NUMBER: 09/367,833
? PRIOR FILING DATE: 1998-08-25
? PRIOR APPLICATION NUMBER: PCT/JP98/00831
? PRIOR FILING DATE: 1998-02-27
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 5
? LENGTH: 180
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: Amino acid sequence of HM1.24 antigen
US-09-760-723-5

```

Query Match	100.0%;	Score 854;	DB 9;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 2e-74;		
Matches 172;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	MASTSYDYCRVPEMEDD	KRCKLLGILGILVLLIIVILCVPLIPIFTKANSACGD	GLRAV	60
Db	1	MASTSYDYCRVPEMEDD	KRCKLLGILGILVLLIIVILCVPLIPIFTKANSACGD	GLRAV	60
Qy	61	MECRANTHLLQDELTEAKG	FQDVEAQAATCNHTMVALMASLDAEKAQGGKVEELGEI		120
Db	61	MECRANTHLLQDELTEAKG	FQDVEAQAATCNHTMVALMASLDAEKAQGGKVEELGEI		120
Qy	121	TTLNHTKLDASAEVERLR	RENOVLSTRIADKKYYSSODSSGAAPOLLIVL		172
Db	121	TTLNHTKLDASAEVERLR	RENOVLSTRIADKKYYSSODSSGAAPOLLIVL		172

RESULT 3  
US-09-355-925-5  
; Sequence 5, Application US/09355925  
; Patent No. US20020037288A1  
; General INFORMATION

Query Match	100.0%;	Score 854;	DB 9;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 2e-74;		
Matches 172;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	MASTSYDVCYRVEMEDODKRC	KLLIGI	GLVLLII	VIIGVPLII	PTIYANSACDGI	RAV	60
Db	1	MASTSYDVCYRVEMEDODKRC	KLLIGI	GLVLLII	VIIGVPLII	PTIYANSACDGI	RAV	60
Qy	61	MECRNATHLLQOELTEAOKG	FODVAZAA	TCNHTYMA	LMDLDEKXQOGK	VELEGEI		120
Db	61	MECRNATHLLQOELTEAOKG	FODVAZAA	TCNHTYMA	LMDLDEKXQOGK	VELEGEI		120
Qy	121	TTLNHKLQDASAEVRLRENO	VSIRIADK	KYYPSSODSSAA	POLLIVL			172
Db	121	TTLNHKLQDASAEVRLRENO	VSIRIADK	KYYPSSODSSAA	POLLIVL			172

RESULT 4  
 US-09-818-648-1  
 Sequence 1, Application US/09818648  
 Patent No. US20020161190A1  
 GENERAL INFORMATION:  
 APPLICANT: HIRANO, TOSHIO  
 KAISHO, TSUNEYASU  
 TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING  
 PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
 P.C.  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/818,648  
 FILING DATE: 28-Mar-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/624,650  
 FILING DATE: 22-MAY-1996  
 APPLICATION NUMBER: PCT/JP94/01732

FILING DATE: 14-OCT-1994  
 APPLICATION NUMBER: JP 5-281622  
 FILING DATE: 15-OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 7625-001-0 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 180 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-818-648-1

Query Match 100.0%; Score 854; DB 9; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFTIKANSEACRDGLRAV 60  
 |||||  
 Db 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFTIKANSEACRDGLRAV 60  
 Qy 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 |||||  
 Db 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 Qy 121 TTLNHNKIQDASAEVERLRERNOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172  
 |||||  
 Db 121 TTLNHNKIQDASAEVERLRERNOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 5  
 US-09-269-921-129  
 Sequence 129, Application US/09269921  
 Publication No. US20030045691A1  
 GENERAL INFORMATION:  
 APPLICANT: Ono, Koichiro  
 APPLICANT: Ohtomo, Toshihiko  
 APPLICANT: Tsuchiya, Masayuki  
 APPLICANT: Yoshimura, Yasuo  
 APPLICANT: Koshimura, Yasuo  
 TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
 FILE REFERENCE: 35029-20007.00  
 CURRENT APPLICATION NUMBER: US/09/269,921  
 EARLIER FILING DATE: 1999-04-01  
 EARLIER APPLICATION NUMBER: PCT/JP97/03553  
 EARLIER FILING DATE: 1997-10-03  
 EARLIER APPLICATION NUMBER: JP 8-264756  
 NUMBER OF SEQ ID NOS: 137  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO 129  
 LENGTH: 180  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
 OTHER INFORMATION: of HM 1.24 antigen  
 US-09-269-921-129

Query Match 100.0%; Score 854; DB 10; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFTIKANSEACRDGLRAV 60  
 |||||  
 Db 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFTIKANSEACRDGLRAV 60

Qy 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 |||||  
 Db 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 Qy 121 TTLNHNKIQDASAEVERLRERNOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172  
 |||||  
 Db 121 TTLNHNKIQDASAEVERLRERNOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 6  
 US-09-509-098-129  
 Sequence 129, Application US/09509098  
 Publication No. US20030103970A1  
 GENERAL INFORMATION:  
 APPLICANT: TSUCHIYA, MASAYUKI  
 TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
 FILE REFERENCE: 053466/0274  
 CURRENT APPLICATION NUMBER: US/09/509,098  
 CURRENT FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: PCT/JP98/04469  
 PRIOR FILING DATE: 1998-10-02  
 PRIOR APPLICATION NUMBER: JP 9-271726  
 NUMBER OF SEQ ID NOS: 203  
 SOFTWARE: Patent In Ver. 2.1  
 SEQ ID NO 129  
 LENGTH: 180  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: HM1.24 antigenic protein  
 US-09-509-098-129

Query Match 100.0%; Score 854; DB 10; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFTIKANSEACRDGLRAV 60  
 |||||  
 Db 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFTIKANSEACRDGLRAV 60  
 Qy 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 |||||  
 Db 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 Qy 121 TTLNHNKIQDASAEVERLRERNOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172  
 |||||  
 Db 121 TTLNHNKIQDASAEVERLRERNOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 7  
 US-10-114-893-46  
 Sequence 46, Application US/10114893  
 Publication No. US20020193567A1  
 GENERAL INFORMATION:  
 APPLICANT: Jacobs, Kenneth  
 APPLICANT: McCoy, John M.  
 APPLICANT: Lavalie, Edward R.  
 APPLICANT: Collins-Racie, Lisa A.  
 APPLICANT: Evans, Cheryl  
 APPLICANT: Merberg, David  
 APPLICANT: Treacy, Maurice  
 APPLICANT: Bowman, Michael R.  
 APPLICANT: Spaulding, Vikki  
 APPLICANT: Carlin-Duckett, McKeough  
 APPLICANT: Kelleher, Kerry S.  
 APPLICANT: Genetics Institute, Inc.  
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 FILE REFERENCE: GI 6000-10A  
 CURRENT APPLICATION NUMBER: US/10/114,893  
 CURRENT FILING DATE: 2002-04-02  
 EARLIER APPLICATION NUMBER: 09/413,232

EARLIER FILING DATE: 1999-10-06  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-114-893-46

Query Match 100.0%; Score 854; DB 13; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDRCKLLIGIIVLIIIVLGPPLIIFITKANSEACRDLRAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGIIVLIIIVLGPPLIIFITKANSEACRDLRAV 60  
QY 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTVWALMASIDAERAKOGKVEELGEI 120  
DB 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTVWALMASIDAERAKOGKVEELGEI 120  
QY 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172  
DB 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

## RESULT 8

US-10-171-311-20  
Sequence 20, Application US/10171311  
Publication No. US20030087270A1  
GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Chen, Yan  
APPLICANT: Zhao, Xumei  
APPLICANT: Monahan, John  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Glatt, Karen  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Hoersch, Sebastian  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
FILE REFERENCE: MRI-035  
CURRENT APPLICATION NUMBER: US/10/171,311  
CURRENT FILING DATE: 2002-06-12  
PRIOR APPLICATION NUMBER: US 60/298,159  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/298,155  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/335,936  
PRIOR FILING DATE: 2001-11-14  
NUMBER OF SEQ ID NOS: 238  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-171-311-20

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDRCKLLIGIIVLIIIVLGPPLIIFITKANSEACRDLRAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGIIVLIIIVLGPPLIIFITKANSEACRDLRAV 60  
QY 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTVWALMASIDAERAKOGKVEELGEI 120  
DB 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTVWALMASIDAERAKOGKVEELGEI 120  
QY 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172  
DB 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

DB 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

## RESULT 9

US-10-315-125-5  
Sequence 5, Application US/10315125  
Publication No. US2003011334A1  
GENERAL INFORMATION:  
APPLICANT: KOISHIHARA, YASUO  
APPLICANT: KOISHIHARA, YASUSHI  
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS  
FILE REFERENCE: 053466/0255  
CURRENT APPLICATION NUMBER: US/10/315,125  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: US/09/355,925  
PRIOR FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: PCT/J998/00568  
PRIOR FILING DATE: 1998-02-12  
PRIOR APPLICATION NUMBER: JP 9-41410  
PRIOR FILING DATE: 1997-02-12  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of Hm1.24 antigen  
US-10-315-125-5

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDRCKLLIGIIVLIIIVLGPPLIIFITKANSEACRDLRAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGIIVLIIIVLGPPLIIFITKANSEACRDLRAV 60  
QY 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTVWALMASIDAERAKOGKVEELGEI 120  
DB 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTVWALMASIDAERAKOGKVEELGEI 120  
QY 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172  
DB 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

## RESULT 10

US-10-218-253-129  
Sequence 129, Application US/10218253  
Publication No. US20030129185A1  
GENERAL INFORMATION:  
APPLICANT: Ono, Koichihiro  
APPLICANT: Ohtomo, Toshiniko  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yoshimura, Yasuaki  
APPLICANT: Koishihara, Yasuo  
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
FILE REFERENCE: 35029-2007.00  
CURRENT APPLICATION NUMBER: US/10/218,253  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US/09/269,921  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: PCT/J997/03553  
PRIOR FILING DATE: 1997-10-03  
PRIOR APPLICATION NUMBER: JP 8-264756  
PRIOR FILING DATE: 1996-10-04  
NUMBER OF SEQ ID NOS: 137  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 129  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Artificial Sequence

QY 1 MASTSYDYCRVPMEDGDRCKLLIGIIVLIIIVLGPPLIIFITKANSEACRDLRAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGIIVLIIIVLGPPLIIFITKANSEACRDLRAV 60  
QY 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTVWALMASIDAERAKOGKVEELGEI 120  
DB 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTVWALMASIDAERAKOGKVEELGEI 120  
QY 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172  
DB 121 TTNHKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
OTHER INFORMATION: of HM 1.24 antigen  
US-10-218-253-129

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFITKANSEACRDLAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFITKANSEACRDLAV 60  
QY 61 MECAVTHLLQOELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGQKKVEELGEI 120  
DB 61 MECAVTHLLQOELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGQKKVEELGEI 120  
QY 121 TTLNHLKODASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172  
DB 121 TTLNHLKODASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 11  
US-10-024-298A-91  
Sequence 91, Application US/10024298A  
Publication No. US20030143540A1  
GENERAL INFORMATION:  
APPLICANT: ASAMI KASEI KABUSHIKI KAISHA  
APPLICANT: AKIO MATSUDA  
APPLICANT: Goichi HONDA  
APPLICANT: Shuji MURAMATSU  
APPLICANT: Yukiko NAGANO  
TITLE OF INVENTION: NF-K B Activating Gene  
FILE REFERENCE: 1254-0191P  
CURRENT APPLICATION NUMBER: US/10/024,298A  
CURRENT FILING DATE: 2003-04-08  
PRIOR APPLICATION NUMBER: 60/314,385  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 60/278,641  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: 60/258,315  
PRIOR FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: JP254018/2001  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: JP0088912/2001  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: JP402288/2000  
PRIOR FILING DATE: 2000-12-28  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 91  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-024-298A-91

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFITKANSEACRDLAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFITKANSEACRDLAV 60  
QY 61 MECAVTHLLQOELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGQKKVEELGEI 120  
DB 61 MECAVTHLLQOELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGQKKVEELGEI 120  
QY 121 TTLNHLKODASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172  
DB 121 TTLNHLKODASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 12  
US-10-042-211A-91  
Sequence 91, Application US/10042211A  
Publication No. US20030170719A1  
GENERAL INFORMATION:  
APPLICANT: MATSUDA, AKIO et al.  
TITLE OF INVENTION: NFkB Activating Gene  
FILE REFERENCE: 1254-0192P  
CURRENT APPLICATION NUMBER: US/10/042,211A  
CURRENT FILING DATE: 2002-01-11  
PRIOR APPLICATION NUMBER: JP 2000-402288  
PRIOR FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: JP 2001-088912  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: JP 2001-254018  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/258,315  
PRIOR FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: US 60/278,640  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: US 60/314,385  
PRIOR FILING DATE: 2001-08-24  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 91  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-042-211A-91

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFITKANSEACRDLAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFITKANSEACRDLAV 60  
QY 61 MECAVTHLLQOELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGQKKVEELGEI 120  
DB 61 MECAVTHLLQOELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGQKKVEELGEI 120  
QY 121 TTLNHLKODASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172  
DB 121 TTLNHLKODASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 13  
US-10-428-085-5  
Sequence 5, Application US/10428085  
Publication No. US20030175281A1  
GENERAL INFORMATION:  
APPLICANT: KOSAKA, MASAAKI  
APPLICANT: KOISHIHARA, YASUO  
TITLE OF INVENTION: ENHANCER FOR ANTIBODY TO LYMPHOCTIC TUMORS  
FILE REFERENCE: 053466/0276  
CURRENT APPLICATION NUMBER: US/10/428,085  
CURRENT FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: US/09/509,530B  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: PCT/JP98/04645  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: JP 10-222024  
PRIOR FILING DATE: 1998-08-05  
PRIOR APPLICATION NUMBER: JP 9-280759  
PRIOR FILING DATE: 1997-10-14  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-428-085-5

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFITKANSEACRDLAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVILGVPPLIIFITKANSEACRDLAV 60  
QY 61 MECAVTHLLQOELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGQKKVEELGEI 120  
DB 61 MECAVTHLLQOELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOGQKKVEELGEI 120  
QY 121 TTLNHLKODASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172  
DB 121 TTLNHLKODASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

Query Match 100.0%; Score 854; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 DB 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 QY 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
 DB 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
 QY 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172  
 DB 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172

## RESULT 14

US-10-423-007-3  
 Sequence 3, Application US/10423007  
 Publication No. US20030180889A1  
 GENERAL INFORMATION:

APPLICANT: OHTOMO, TOSHIHIKO  
 APPLICANT: TSUCHIYA, MASAYUKI  
 APPLICANT: KOISHIHARA, YASUO  
 APPLICANT: KOSAKA, MASAAKI  
 TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND  
 FILE REFERENCE: 053466/0285  
 CURRENT FILING DATE: 2003-04-25  
 PRIOR FILING DATE: 2003-04-25  
 PRIOR APPLICATION NUMBER: US/09/622,166A  
 PRIOR FILING DATE: 2000-08-14  
 PRIOR APPLICATION NUMBER: PCT/JP99/00884  
 PRIOR FILING DATE: 1999-02-25  
 PRIOR APPLICATION NUMBER: 10-60617  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 10-93883  
 PRIOR FILING DATE: 1998-03-24  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 180  
 TYPE: PRT  
 ORGANISM: Mus sp.

US-10-423-007-3

Query Match 100.0%; Score 854; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 DB 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 QY 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
 DB 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
 QY 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172  
 DB 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172

## RESULT 15

US-10-257-021-80  
 Sequence 80, Application US/10257021  
 Publication No. US20030211498A1  
 GENERAL INFORMATION:

APPLICANT: Morin, Patrice J.  
 APPLICANT: Sherman-Baust, Cheryl A.  
 APPLICANT: Pfizer, Ellen S.

APPLICANT: Hough, Colleen D.  
 TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER  
 FILE REFERENCE: 14014.0369U2  
 CURRENT APPLICATION NUMBER: US/10/257,021  
 CURRENT FILING DATE: 2002-10-03  
 PRIOR APPLICATION NUMBER: PCT/US01/10947  
 PRIOR FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: 60/194,336  
 PRIOR FILING DATE: 2000-04-03  
 NUMBER OF SEQ ID NOS: 147  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 80  
 LENGTH: 180  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-10-257-021-80

Query Match 100.0%; Score 854; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 DB 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 QY 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
 DB 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
 QY 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172  
 DB 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172

Search completed: December 29, 2004, 11:41:12  
 Job time : 589 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 11:11:07 ; Search time 25 Seconds  
(without alignments)  
661.971 Million cell updates/sec

Title: US-10-069-290A-2  
Perfect score: 854  
Sequence: 1 MASTSYDYCRVPMEDGDKRC.....YTPSSQDSSAAAPQLLIVL 172

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	854	100.0	180	2	A56836 bone marrow stroma
2	111	13.0	778	2	T30430 hypothetical prote
3	107.5	12.6	461	2	H84099 cell wall-binding
4	107	12.5	143	2	G83955 flagellar protein
5	104	12.2	423	2	I59463 keratin, type I, c
6	102.5	12.0	1534	2	A56734 ribosome receptor,
7	101.5	11.9	550	2	A28166 Kupffer cell recep
8	99.5	11.7	304	2	JY0209 lectin, galactose/
9	99	11.6	415	2	S35760 fcrA protein preu
10	98.5	11.5	1963	1	MMKW myosin heavy chain
11	98	11.5	1938	1	AMWKM1 myosin heavy chain
12	98	11.5	1938	1	A59293 myosin heavy chain
13	97	11.4	286	2	S07533 puf II/9A-2 prote
14	96.5	11.3	597	2	S40998 hypothetical prote
15	96.5	11.3	893	2	G88551 protein M01A8.2 (I
16	96	11.2	286	2	S07532 puf II/9-1 protei
17	95	11.1	1937	2	I38055 myosin heavy chain
18	95	11.1	1972	1	A41604 myosin heavy chain
19	94.5	11.1	173	2	S76705 hypothetical prote
20	94	11.0	676	2	S00084 myosin heavy chain
21	93.5	10.9	140	2	H64629 hypothetical prote
22	93	10.9	359	2	I50712 TOP AP - chicken
23	93	10.9	848	2	A44972 paramyosin - nemat
24	93	10.9	879	2	A48575 paramyosin - nemat
25	93	10.9	1938	2	JC5420 smooth muscle myos
26	93	10.9	1972	2	JC5420 smooth muscle myos
27	92.5	10.8	1972	2	G95258 secreted 45 kd pro
28	92.5	10.8	392	2	B98124 general stress pro
29	92.5	10.8	1388	2	S74245 serine/threonine-s

30	92.5	10.8	1938	1	S06005 myosin alpha heavy
31	92.5	10.8	1939	2	I48175 myosin heavy chain
32	92	10.8	866	2	S04027 paramyosin - Caero
33	92	10.8	872	2	T19296 hypothetical prote
34	91.5	10.7	746	2	T47237 myosin II heavy ch
35	91.5	10.7	1938	2	I49464 alpha cardiac myos
36	91.5	10.7	2442	2	T08621 centrosome associa
37	91	10.7	507	2	S05542 hypothetical prote
38	91	10.7	741	2	S39082 myosin heavy chain
39	91	10.7	955	2	S24348 myosin heavy chain
40	90.5	10.6	244	2	I6913 beta-myosin heavy
41	90.5	10.6	764	2	I51302 myosin heavy chain
42	90.5	10.6	1039	2	S18199 myosin heavy chain
43	90.5	10.6	1509	1	A27224 myosin heavy chain
44	90.5	10.6	1846	2	A59289 myr 6, unconvecto
45	90.5	10.6	1934	2	I48153 myosin heavy chain

## ALIGNMENTS

```
RESULT 1
A56836
bone marrow stromal cell surface protein BST-2 - human
C:Species: Homo sapiens (man)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56836
R:Rishikawa, J.; Kaisho, T.; Tomizawa, H.; Lee, B.O.; Kobune, Y.; Inazawa, J.; Oritani, K.
Genomics 26, 527-534, 1995
A>Title: Molecular cloning and chromosomal mapping of a bone marrow stromal cell surface
A:Reference number: A56836; MUID:95331788; PMID:7607676
A:Accession: A56836
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-180 <ISH>
A:Cross-references: UNIPROT:Q10589; GB:D28137; NID:9457563; PID:BAA05679.1; PID:G506861
C:Genetics:
A:Gene: GDB:BST2
A:Cross-references: GDB:409946; OMIM:600534
A:Map position: 19p13.2-19p13.2
C:Keywords: transmembrane protein

Query Match      100.0%; Score 854; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.2e-60;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASTSYDYCRVPMEDGDKRCALLIGILVLLIIVIGVPIIFTIKANSEACRDGLRAV 60
DB      1 MASTSYDYCRVPMEDGDKRCALLIGILVLLIIVIGVPIIFTIKANSEACRDGLRAV 60
QY      61 MECNNVTHLLQOELTEAKGQDVEAOATCNHTVMMAISLDEKAGQKVEELBGEI 120
DB      61 MECNNVTHLLQOELTEAKGQDVEAOATCNHTVMMAISLDEKAGQKVEELBGEI 120
QY      121 TTNHKKLQDASAEYERLRRENOVLSVRADKKYTPSSQDSSAAAPQLLIVL 172
DB      121 TTNHKKLQDASAEYERLRRENOVLSVRADKKYTPSSQDSSAAAPQLLIVL 172

RESULT 2
T30430
hypothetical protein ORF42 - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30430
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
Virology 253, 17-34, 1999
A>Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30430
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-778 <KUZ>
```





## RESULT 6

A56734  
ribosome receptor, 180k - dog  
C:Species: Canis lupus familiaris (dog)  
C>Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: A56734  
J:Marker, E.E.; Sun, Y.; Savltz, A.J.; Meyer, D.I.  
J:Cell Biol. 130, 29-39, 1995  
A:Title: Functional characterization of the 180-kD ribosome receptor in vivo.  
A:Reference number: A56734; MUID:95310363; PMID:7790375  
A:Accession: A56734  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1534 <MAN>  
A:Cross-references: UNIPROT:Q28298; GB:X87224; NID:984113; PIDN:CAA6076.1; PID:984114  
C:Keywords: endoplasmic reticulum; membrane protein; protein biosynthesis  
F:198-743/Region: 10-residue repeats (N-Q-G-K-K-A-E-G-A-P)

Query Match 12.0%; Score 102.5; DB 2; Length 1534;  
Best Local Similarity 28.6%; Pred. No. 3.6;

Matches 26; Conservative 22; Mismatches 42; Indels 1; Gaps 1;

Qy 55 DGLRAWECRNVTNHLQDELTEAOKGFODVEAQAATCNHTWALMASLDAEKAQCKYVE 114  
Db 847 DAAVAKSKLRVNNKELAAEKAKAAAGKAKVKQLVARBOETVAQARIEASYREHVEQV 906  
Qy 115 ELBEGITTLNHLKODA-SAEVERLARENQVL 144  
Db 907 QLOGKIRTLQEOLENGPNTQLARLQOENSIL 937

## RESULT 7

A28166  
Kupffer cell receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
C:Accession: A28166  
J:Hoyle, G.W.; Hill, R.L.  
J: Biol. Chem. 266, 1850-1857, 1991  
A:Title: Structure of the gene for a carbohydrate-binding receptor unique to rat Kupffer  
A:Reference number: A28166; MUID:91107689; PMID:1846367  
A:Accession: A28166  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-550 <HO2>  
A:Cross-references: UNIPROT:P10716; GB:M55532; NID:9203362; PIDN:AAA40892.1; PID:9203363  
J:Hoyle, G.W.; Hill, R.L.  
J: Biol. Chem. 263, 7487-7492, 1988  
A:Title: Molecular cloning and sequencing of a cDNA for a carbohydrate binding receptor  
A:Reference number: A28166; MUID:88227939; PMID:2836387  
A:Accession: A28166  
A:Molecule type: mRNA  
A:Residues: 1-550 <HOY>  
A:Cross-references: GB:J03734; NID:9205050; PIDN:AAA41472.1; PID:9205051  
C:Keywords: transmembrane protein  
F:412-536/Domain: C-type lectin homology <LCH>

Query Match 11.9%; Score 101.5; DB 2; Length 550;  
Best Local Similarity 26.0%; Pred. No. 1.5;

Matches 32; Conservative 22; Mismatches 58; Indels 11; Gaps 2;

Qy 46 IKANEACRQDGLRAWECRNVTNHLQDELTEAOKGFODVEAQAATCNHTWALMASLDAE 105  
Db 256 ISAEIQARQDGMQRGE-----EWTSLKQLELTITTAQIQANGLBETDTQIQGL 305  
Qy 106 KAQCGKVELEGETITTLNHLKODASAEVERLARENQVL SVRIADKCYPPSQDSSSAA 165  
Db 306 KAQ- LKSTSSINSQLEVVNGKLDSSRELQTLRRDLSDVSALKSNVQMLQAKAKAV 364  
Qy 166 PQL 168  
Db 365 QSL 367

## RESULT 8

UX0209  
lectin, galactose/N-acetylglactosamine-specific - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: UX0209; PX0009  
J:Sato, M.; Kawakami, K.; Osawa, T.; Toyoshima, S.  
J: Biochem. 111, 331-336, 1992  
A:Title: Molecular cloning and expression of cDNA encoding a galactose/N-acetylglactosa  
A:Reference number: UX0209; MUID:92268032; PMID:1587794  
A:Accession: UX0209  
A:Molecule type: mRNA  
A:Residues: 1-304 <SAT>  
A:Cross-references: UNIPROT:P49300; GB:S36676; NID:9249360; PIDN:AAB22171.1; PID:9249361  
J:Roda, S.; Sato, M.; Toyoshima, S.; Osawa, T.  
J: Biochem. 104, 600-605, 1988  
A:Title: Purification and characterization of a lectin-like molecule specific for galact  
A:Reference number: PX0009; MUID:89197865; PMID:3241002  
A:Accession: PX0009  
A:Molecule type: protein  
A:Residues: 102-120:137 'X', 139-151 <ODA>  
C:Superfamily: hepatic lectin; C-type lectin homology  
C:Keywords: glycoprotein; lectin; macrophage; transmembrane protein  
F:36-61/Domain: transmembrane #status predicted <TRA>  
F:173-296/Domain: C-type lectin homology <LCH>  
F:74.166/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 11.7%; Score 99.5; DB 2; Length 304;  
Best Local Similarity 23.2%; Pred. No. 1.2;

Matches 36; Conservative 37; Mismatches 49; Indels 33; Gaps 7;

Qy 24 LGIGLVTLIVLIGVPLIFITKANSEACRD--GLRAWECRNVTNHLQDELTEAOKGF 81  
Db 41 LGLSLILVAVSVIG-----SNGSLRDLGLTRKTLTD--NTSKIKAE-----F 83  
Qy 82 QDVEAQAATCNHTWALMASLDAEKAQCKYVELEGETI-----TTNHLKODAS 131  
Db 84 QSLDRADSPFEKGISLKVDEVDHROQLQAGRDLQKVTSLSTVEKREQLKTDLSLT 143  
Qy 132 AEVERLARENQVL SVRIADKCYPPSQDSSSAAAP 166  
Db 144 DHVQQLRKALKTQLANLK---NNGSEVACCP 174

## RESULT 9

S35760  
ferritin precursor - Streptococcus pyogenes  
C:Species: Streptococcus pyogenes  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S35760; A42711  
J:Podbielski, A.  
submitted to the EMBL Data Library, November 1992  
A:Reference number: S35760  
A:Accession: S35760  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-415 <POD>  
A:Cross-references: UNIPROT:O54859; EMBL:X69324; NID:9311759; PIDN:CAA49165.1; PID:93117  
J:Haanes, E.J.; Heath, D.G.; Cleary, P.P.  
J: Bacteriol. 174, 4967-4976, 1992  
A:Title: Architecture of the vir regulons of group A streptococci parallels opacity fact  
A:Reference number: A42711; MUID:92332431; PMID:1385809  
A:Accession: A42711  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 343-415 <HAA>  
A:Cross-references: GB:M66806; NID:9153630; PIDN:AAA26887.1; PID:9153631  
A:Experimental source: strain CS101, OF+  
A>Note: sequence extracted from NCI backbone (NCBIN:108942, NCBIPI:108945)  
C:Superfamily: M5 protein

Query Match 11.6%; Score 99; DB 2; Length 415;



F:764-778/Region: actin binding #status predicted  
F:846-1938/Domain: coiled coil #status predicted <COT>  
F:846-1160/Region: S2  
F:1161-1938/Region: light meromyosin  
F:1126/Modified site: N6/N6-trimethyllysine (lys) #status predicted  
F:189/Binding site: ATP (lys) #status predicted  
F:700,710/Active site: Cys #status predicted

Query Match 11.5%; Score 98; DB 1; Length 1938;  
Best Local Similarity 26.6%; Pred. No. 10;  
Matches 34; Conservative 24; Mismatches 58; Indels 12; Gaps 4;

QY 51 EACRDLRAVME---CNRVTHLQQ--ELTEAQ-KGFQDVEAQAATCNHTVMALMSID 103  
Db 1324 KAABDELHERQEFNAACNLEHLDQCHLEEQINGKDIQRLSRINSEISQWKARYE 1383  
QY 104 AEKAGQCKVKELEGEITTLNHLQDASAEVRLRENOVSVRLADKKYVSSODSSA 163  
Db 1384 GEGVSESELEELKKNRMVMDLQELASAA-----QNKVLSLEKAKGLLAETEDARS 1438  
QY 164 AAPQLLIV 171  
Db 1439 VDRHLTVI 1446

## RESULT 12

A59293  
skeletal myosin heavy chain - domestic rabbit  
C:Species: Oryctolagus cuniculus  
C>Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: A59293  
R:Maeda, K.; Hostinova, E.; Roesc, Kleinkauf, A.; Schuster, H.; Gasperik, J.; Wittinghofer  
submitted to GenBank, July 1995  
A:Description: Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal mus  
A:Reference number: A59293  
A:Accession: A59293  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1938 <MAE>  
A:Cross-references: UNIPROT:028641; GB:U3574; NID:G940232; PIDN:AAAT4199.1; PID:G94023  
A:Experimental source: strain New Zealand White; cell type skeletal muscle fiber type II  
C:Genetics:  
A:Gene: MYH  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
F:89-769/Domain: myosin motor domain homology <MMO>

Query Match 11.5%; Score 98; DB 2; Length 1938;  
Best Local Similarity 26.1%; Pred. No. 10;  
Matches 37; Conservative 20; Mismatches 45; Indels 40; Gaps 5;

QY 47 KANSEACR-----DGLRAVMECRNVTHLQOELTEAQKGFQDVEAQAATCNHTVMALM 99  
Db 1366 KANSEVAQWRKRYETDAIQRTLEAEAKKLAQRLQDAE---EHYEAVNAKC----- 1414  
QY 100 ASLDAEKAQCKVKELEGEITTLN-----HKLQDASAEVERLR 138  
Db 1415 ASLEKTKQRLQNEVDLMIDVERTNAACALDKQRFNFDKILAEWKHYETHALELSQ 1474  
QY 139 RENQVLSVRIAD-KKYVPSQD 159  
Db 1475 KESRSLSTVFVKVNAYESLD 1496

## RESULT 13

S07533  
puff II/9A-2 protein precursor - fungus gnat (Sciara coprophila)  
C:Species: Sciara coprophila  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: S07533  
R:DiBarcolomeis, S.M.; Gerbi, S.A.  
J. Mol. Biol. 210, 531-540, 1989  
A>Title: Molecular characterization of DNA puff II/9A genes in Sciara coprophila.  
A:Reference number: S07532; MUID:90133907; PMID:2614832

A:Accession: S07533  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-286 <DIB>  
A:Cross-references: UNIPROT:P22312; GB:X51679; NID:G10113; PID:G1405812

C:Genetics:  
A:Map position: II/9A  
C:Keywords: coiled coil; glycoprotein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-286/Product: puff II/9A protein #status predicted <MAT>  
F:156/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 11.4%; Score 97; DB 2; Length 286;  
Best Local Similarity 25.6%; Pred. No. 1.8;  
Matches 31; Conservative 24; Mismatches 36; Indels 30; Gaps 5;

QY 46 IKANSEACRDLRAVMECRNVTHLQOELTEAQKGFQDVEAQAATCNHTVMAL 98  
Db 89 LKREKARQKAEKAEQKATENKETTLEQLKSLARQALKCKELADCK----- 142  
QY 99 MASLDAEKAQCKVKELEGEITTLNHLQ-----DASAEVERLRRE---NQVLSV 146  
Db 143 -----KENAKLNTKTEELNCTITTOLEKLERGRGRRLQQLDCKKKKNTCNNEELAC 197  
QY 147 R 147  
Db 198 R 198

## RESULT 14

S40998  
hypothetical protein M01A8.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S40998  
R:Hawkins, T.; Thomas, K.  
submitted to the EMBL Data Library, October 1993  
A:Reference number: S40997  
A:Accession: S40998  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-597 <HAN>  
A:Cross-references: EMBL:Z27081  
C:Genetics:  
A:introns: 40/3; 76/1; 125/1; 199/1; 240/1; 274/1; 292/3; 392/3; 429/2; 486/2; 521/1

Query Match 11.3%; Score 96.5; DB 2; Length 597;  
Best Local Similarity 24.8%; Pred. No. 4.1;  
Matches 32; Conservative 29; Mismatches 39; Indels 29; Gaps 4;

QY 48 ANSEACRDLRAVMECRNVTHLQOELTEAQKGFQDVEAQAATCNHTVMALMS 101  
Db 270 SNOQVIRHANAV-ESLQKTHETQIAEKKEPERNFEEARARRAEVCAMNRHQKVAC 328  
QY 102 LDAEKAQCKVKELE-----GEITTLNHLQDASAEVERLR 139  
Db 329 IDEKISEAKQCEQLNVQKVLQALANDCDHRNQMTKTEISLQFALEMSAAEMKEIRQ 388  
QY 140 ENQVLSVRI 148  
Db 389 KNQNLISQV 397

## RESULT 15

G88551  
protein M01A8.2 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: G88551  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; MUID:93069613; PMID:9851916



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 11:31:07 / Search time 104 Seconds

(without alignments)  
951.581 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854  
Sequence: 1 MASTSYDYCRVPMEDGDRRC.....YYPSSQDSSAAAPQLITVL 172

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_prot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854	100.0	180	1 BSTR2 HUMAN	Q10589 homo sapien
2	297.5	34.8	203	2 O6WRUO	Q6WRUO cricetulus
3	297.5	34.8	203	2 AaQ16301	AaQ16301 cricetulu
4	271	31.7	172	2 O8R2Q8	O8R2Q8 mus musculu
5	229.5	26.9	172	2 O811A2	O811A2 rattus norv
6	162.5	19.0	108	2 O8CEY7	O8CEY7 mus musculu
7	111	13.0	778	2 O9YMP5	O9YMP5 lymantria d
8	107.5	12.6	461	2 O9K6X4	O9K6X4 bacillus ha
9	107	12.5	143	2 O9KX43	O9KX43 bacillus ha
10	104.5	12.2	560	2 O7ZTT2	O7ZTT2 brachydanio
11	104.5	12.2	782	1 HCR_PANPA	O8H57 pan paniscu
12	104.5	12.2	782	1 HCR_PANTR	O8H260 pan troglod
13	104	12.1	900	2 O7R6H3	O7R6H3 giardia lam
14	103	12.1	782	1 HCR_PONPY	O8H258 pongo pygma
15	102.5	12.0	621	2 O7Q003	O7Q003 giardia lam
16	102.5	12.0	1534	2 R8R1 CANPA	O28298 canis famli
17	102.5	12.0	1627	2 O7R264	O7R264 giardia lam
18	102.5	12.0	1627	2 O962Q0	O962Q0 giardia lam
19	101.5	11.9	304	2 O91Y73	O91Y73 mus musculu
20	101.5	11.9	507	2 O8CHM5	O8CHM5 mus musculu
21	101.5	11.9	526	2 O8CB50	O8CB50 mus musculu
22	101.5	11.9	550	1 KUCR_RAT	P10716 rattus norv
23	101.5	11.9	782	1 HCR_HUMAN	O8C31 homo sapien
24	101.5	11.9	826	1 O9YHDS	O9YHDS rana catesb
25	101	11.8	782	1 HCR_GORGO	O8H59 gorilla gor
26	101	11.8	782	2 O76SHO	O76SHO homo sapien
27	101	11.8	782	2 BAD05130	BAD05130 homo sapi
28	101	11.8	782	2 BAD05131	BAD05131 homo sapi
29	100	11.7	865	2 O96SN6	O96SN6 gallus gall
30	99.5	11.7	270	2 P79391	P79391 bos taurus
31	99.5	11.7	304	1 MMGL_MOUSE	P49300 mus musculu

32	99.5	11.7	304	2 AAD31028	AAD31028 mus muscu
33	99.5	11.7	708	2 O9YHD7	O9YHD7 rana catesb
34	99.5	11.7	980	2 O73ML2	O73ML2 treponema d
35	99.5	11.7	980	2 AAS12013	AAS12013 treponema
36	99.5	11.7	1130	2 O861C6	O861C6 dictyosteli
37	99.5	11.7	1622	2 O80224	O80224 brachydanio
38	99.5	11.7	1932	2 O98TQ4	O98TQ4 notothenia
39	99	11.6	415	2 O54859	O54859 streptococc
40	99	11.6	800	2 O96X03	O96X03 emericellia
41	98.5	11.5	601	2 O6CUP5	O6CUP5 gasteroste
42	98.5	11.5	601	2 AAS19755	AAS19755 gasterost
43	98.5	11.5	782	2 O61AC8	O61AC8 homo sapien
44	98.5	11.5	782	2 CAG33508	CAG33508 homo sapi
45	98.5	11.5	975	2 O98TQ5	O98TQ5 notothenia

## ALIGNMENTS

### RESULT 1

BSTR2\_HUMAN STANDARD; PRT; 180 AA.

AC O10589;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bone marrow stromal antigen 2 (BST-2).  
GN Name=BST2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP

SEQUENCE FROM N.A.  
RX MEDLINE=95331788; PubMed=7607676;  
RA Ishikawa J., Kaiho T., Tomizawa H., Lee B.O., Kobune Y., Inazawa J.,  
RA Ohtani K., Itoh M., Ochi T., Ishihara K., Hirano T.;  
RT "Molecular cloning and chromosomal mapping of a bone marrow stromal  
cell surface gene, BST2, that may be involved in pre-B-cell growth.";  
RL Genomics 26:527-534(1995).  
RN [2]  
RP

SEQUENCE FROM N.A.

RC TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altchul S.F., Zeeberg B., Burow K.H., Scheffer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carinci P., Prange C.,  
RA Paha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U.A.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: May be involved in pre-B-cell growth.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -1- TISSUE SPECIFICITY: Predominantly expressed in liver, lung, heart  
and placenta. Lower levels in pancreas, kidney, skeletal muscle  
and brain.  
CC -1- DISEASE: May play a role in B-cell activation in rheumatoid  
arthritis (RA).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; D28137; AA05679.1; -  
 CC EMBL; BC03873; AAH3873.1; -  
 DR PIR; A56836; A56836.  
 DR Genew; HGNC:1119; BST2.  
 DR MIM: 600534; -  
 DR GO; GO:0005887; C-integral to plasma membrane; TAS.  
 DR GO; GO:0004871; F-signal transducer activity; IEP.  
 DR GO; GO:0008283; P-cell proliferation; TAS.  
 DR GO; GO:0007267; P-cell-cell signaling; TAS.  
 DR GO; GO:0007275; P-development; TAS.  
 DR GO; GO:0006959; P-humoral immune response; TAS.  
 DR GO; GO:0043123; P-positive regulation of I-kappaB kinase/NF-kappaB; IEP.  
 KM Glycoprotein; Polymorphism; Signal-anchor; Transmembrane.  
 FT DOMAIN 1 20 Cytoplasmic (Potential).  
 FT TRANSMEM 21 48 Signal-anchor for type II membrane protein (Potential).  
 FT FT 49 180 Extracellular (Potential).  
 FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).  
 FT VARIANT 143 143 V -> F (in dbSNF:1804402).  
 FT OK FTID=VAR\_012067.  
 SQ SEQUENCE 180 AA; 19769 MW; CAF52340D69061EE CRC64;

Query Match 100.0%; Score 854; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-59;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCVPMEDGDKRCKLLIGILVLLIIVLGPPLIFITKANSEACRDGLAY 60  
 DB 1 MASTSYDYCVPMEDGDKRCKLLIGILVLLIIVLGPPLIFITKANSEACRDGLAY 60  
 QY 61 MERNVTHLLQOELTEAOKGFQVDEAQAATCNHTVMALMSLDAEKAQGGKVEELGEI 120  
 DB 61 MERNVTHLLQOELTEAOKGFQVDEAQAATCNHTVMALMSLDAEKAQGGKVEELGEI 120  
 QY 121 TLTNHLKQDASAEVERLRRENOVLAVRIADKYYPSQDSSAAAPQLLIVL 172  
 DB 121 TLTNHLKQDASAEVERLRRENOVLAVRIADKYYPSQDSSAAAPQLLIVL 172

## RESULT 2

Q6MRUO PRELIMINARY; PRT; 203 AA.

ID O6MRUO;  
 DT 05-JUN-2004 (TREMBlrel. 27, Created)  
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)  
 OS Luminal membrane-associated protein GREG.  
 DE Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OC NCB1\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Li X., Helms J.B.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY272060; AAQ16301.1; -  
 SQ SEQUENCE 203 AA; 22826 MW; 83D2F6B26504B94 CRC64;

Query Match 34.8%; Score 297.5; DB 2; Length 203;  
 Best Local Similarity 35.9%; Pred. No. 1.5e-15;  
 Matches 71; Conservative 35; Mismatches 63; Indels 29; Gaps 4;

QY 1 MASTSYDYCVPMEDGDKRCKLLIGILVLLIIVLGPPLIFITKANSEACRDG 56  
 DB 1 MASTSYDYCVPMEDGDKRCKLLIGILVLLIIVLGPPLIFITKANSEACRDG 56

DB 1 MAPFYHPLPMDQKEPGGIRWRCLAAASVLLVALVI---PLIFAVKANSEACRDG 57  
 QY 57 LRAVMECRNTHLLQOELTEAOKGFQVDEAQAATCNHTVMALMSLDAEKAQGGK---- 112  
 DB 58 LRAVECSNTRRLQRLQRLTSQDNLQAQEAQASCTNRTVTLQDSELEKYSQIOEKAL 117  
 QY 113 -----VELEGEITLTNHLKQDASAEVERLR-----ENQVLSVRIADKYY 154  
 DB 118 QOEAQIKQEAQIKQEAQIKQEAQIKQEAQIKQEAQIKQEAQIKQEAQIKQEAQIK 177  
 QY 155 PSSQDSSAAAPQLLIVL 172  
 DB 178 TSKQNSAGSMVAVSSILVL 195

## RESULT 3

AAQ16301 PRELIMINARY; PRT; 203 AA.

AC AAQ16301;  
 DT 10-MAY-2004 (TREMBlrel. 27, Created)  
 DT 10-MAY-2004 (TREMBlrel. 27, Last sequence update)  
 DT 10-MAY-2004 (TREMBlrel. 27, Last annotation update)  
 OS Luminal membrane-associated protein GREG.  
 OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OC NCB1\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Li X., Helms J.B.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY272060; AAQ16301.1; -  
 SQ SEQUENCE 203 AA; 22826 MW; 83D2F6B26504B94 CRC64;

Query Match 34.8%; Score 297.5; DB 2; Length 203;  
 Best Local Similarity 35.9%; Pred. No. 1.5e-15;  
 Matches 71; Conservative 35; Mismatches 63; Indels 29; Gaps 4;

QY 1 MASTSYDYCVPMEDGDKRCKLLIGILVLLIIVLGPPLIFITKANSEACRDG 56  
 DB 1 MASTSYDYCVPMEDGDKRCKLLIGILVLLIIVLGPPLIFITKANSEACRDG 56  
 QY 57 LRAVMECRNTHLLQOELTEAOKGFQVDEAQAATCNHTVMALMSLDAEKAQGGK---- 112  
 DB 58 LRAVECSNTRRLQRLQRLTSQDNLQAQEAQASCTNRTVTLQDSELEKYSQIOEKAL 117  
 QY 113 -----VELEGEITLTNHLKQDASAEVERLR-----ENQVLSVRIADKYY 154  
 DB 118 QOEAQIKQEAQIKQEAQIKQEAQIKQEAQIKQEAQIKQEAQIKQEAQIKQEAQIK 177  
 QY 155 PSSQDSSAAAPQLLIVL 172  
 DB 178 TSKQNSAGSMVAVSSILVL 195

## RESULT 4

O6R208 PRELIMINARY; PRT; 172 AA.

ID O6R208;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 26, Last annotation update)  
 DE DAMP-1 protein.  
 GN Name=2310015110R1k;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;

QY 1 MASTSYDYCVPMEDGDKRCKLLIGILVLLIIVLGPPLIFITKANSEACRDG 56  
 DB 1 MASTSYDYCVPMEDGDKRCKLLIGILVLLIIVLGPPLIFITKANSEACRDG 56





```

RX MEDLINE=2049374; PubMed=11042159;
RA Carinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [51]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carinci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Taisho H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carinci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hasegaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Konda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T.,
RA Tejlina Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK009361; BAC25254.1; -
DR MGD; MGI:1916800; 231001511ORIK.
KW Hypothetical protein.
FT NON_TER 1
SQ
SEQUENCE 108 AA; 12173 MW; COEADFP2B4117889D CRC64;
Query Match 19.0%; Score 162.5; DB 2; Length 108;
Best Local Similarity 36.5%; Pred. No. 3.2e-05;
Matches 42; Conservative 19; Mismatches 33; Indels 21; Gaps 4;
QY 62 ECGNTHLHQELTEKQKGFQVDEAQAATCNHTVMAISLDEKQG---QKVEELG 118
DB 3 ECGNTHLHQELTEKQKGFQVDEAQAATCNHTVMAISLDEKQG---QKVEELG 62
QY 119 EITLHKLQDASAEYERLRENOVLS-VRADKKTYPSSDSSAAAPOLITVL 172
DB 63 EITLHKLQDASAEYERLRENOVLS-VRADKKTYPSSDSSAAAPOLITVL 100
RESULT 7
Q9YMP5 PRELIMINARY; PRT; 778 AA.
AC Q9YMP5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ldort-82 peptide.
OS Lymantiria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99124785; PubMed=9887315;
RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
RA Slavicek J.M., Rohmann G.F.;
RT "Sequence and analysis of the genome of a baculovirus pathogenic for
RT Lymantiria dispar.";

```

```

RL Virology 253:17-34(1999).
DR EMBL; AF081810; AAC70256.1; -
DR PIR; T30430; T30430; -
DR InterPro; IPR009615; Desmo N.
DR InterPro; IPR010989; t-snare.
DR Pfam; PF06771; Desmo N; 1.
SQ SEQUENCE 778 AA; 87841 MW; 811B8BD172CE9E43 CRC64;
Query Match 13.0%; Score 111; DB 2; Length 778;
Best Local Similarity 32.5%; Pred. No. 2.8;
Matches 38; Conservative 22; Mismatches 47; Indels 10; Gaps 4;
QY 46 IKANSEACRDPGLRAVMEGR-VNTHLLQDELTEAKQGFQVDEAQAATCNHTVMAISLDA 104
DB 520 LKAGSELNRD-LQAKAEQAQANRLQAEIDSLKR---ASDADALNRVAQLAEAEAS 574
QY 105 EKAGQKVEELTEGHTTLNHLQDASAEYERLRENOVLSVRADKKTYPSSDSS 161
DB 575 GAADLQNRILARLEASSGLTRLOESAELVALRDKEDLERRTAAS---AADVS 627
RESULT 8
Q9K6X4 PRELIMINARY; PRT; 461 AA.
AC Q9K6X4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell wall-binding protein.
GN Name=BH3600;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86655;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001519; BAB07319.1; -
DR PIR; H84099; H84099.
DR GO; GO:0004223; F:metalloendopeptidase activity; IEA.
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M23B.
DR InterPro; IPR009061; Putativ_DNA_Bind.
DR InterPro; IPR011054; Rudmut_hyb_motif.
DR Pfam; PF01551; Peptidase_M23; 1.
SQ SEQUENCE 461 AA; 50372 MW; 2918480CD67AF3F CRC64;
Query Match 12.6%; Score 107.5; DB 2; Length 461;
Best Local Similarity 26.1%; Pred. No. 3;
Matches 31; Conservative 28; Mismatches 55; Indels 5; Gaps 2;
QY 33 ITVILGVPLIFTITANSACRDLRAVMEGR-VNTHLLQDELTEAKQGFQVDEAQAATCN 92
DB 5 ISLVAAAGLITTSILFSOSIEDA-KANSSLQNSIDVQKQKQKQKTEAL----- 59
QY 93 HTVMAISLDAEKAGQKVEELTEGHTTLNHLQDASAEYERLRENOVLSVRADK 151
DB 60 KEVEKELGDTAEIRLDRKVEVETSGKIQEKREELIEVQAEIIEELKQETIEERIAER 118
RESULT 9
Q9KA43 PRELIMINARY; PRT; 143 AA.
AC Q9KA43;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```



DE Flagellar protein required for flagellar formation.  
GN Name=flj;  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=8665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125;  
RA MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Ogasawara N., Kuhara S.,  
RA Fuji F., Hirata C., Nakamura Y.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331 (2000).  
DR EMBL, AP001515; BAB06166.1; --  
DR PIR, G83955; G83955.  
DR GO; GO:0009425; C:Flagellar basal body (sensu Bacteria); IEA.  
DR GO; GO:0006935; P:chemotaxis; IEA.  
DR GO; GO:0001539; P:ciliary/flagellar motility; IEA.  
DR InterPro; IPR005503; FILP.  
DR Pfam; PF03748; FILP; 1.  
KW Flagellum.  
SO SEQUENCE 143 AA; 16386 MW; 613446D64B1C5402 CRC64;  
Query Match 12.5%; Score 107; DB 2; Length 143;  
Best Local Similarity 22.1%; Pred. No. 0.99; Indels 26; Gaps 4;  
Matches 31; Conservative 34; Mismatches 49;  
QY 23 LGGIIVLVIIIVLIPVLIIFTIKANSEACRDLRAVMEC-----RVNTHLLOQL 74  
DB 6 LVNIMLIIIVLVTVGVAVLIFVNVFNNEDEQDREPTIDEIQAQSVETREITNLSDNF 65  
QY 75 TEA-----QKGQDVEAQAATGNTHTVMAASLDEKAGQCKVELESEITTLNKK 126  
DB 66 VRARELVHVDNRNALQEVQRDPQVNNIIRSLAGDMSQSLSGADIGETLEAQ----- 118  
QY 127 LODASAEVRLRENOVLSV 146  
DB 119 LQD---DINALMQEGSVVKI 135  
RESULT 10  
Q7ZTT2 PRELIMINARY; PRT; 560 AA.  
ID Q7ZTT2  
AC Q7ZTT2;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Similar to K1A1536 protein.  
GN Name=zgc:56638;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole body;  
RC MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Maitra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole body;  
RC Strausberg R.;  
RL Submitted (Apr-2003) to the EMBL/Genbank/DBJ databases.  
RL EMBL, BC051625; AAH51625.1; --  
DR InterPro; IPR02017; Spectrin.  
SO SEQUENCE 560 AA; 64730 MW; 33CD835C9D9DB8E CRC64;  
Query Match 12.2%; Score 104.5; DB 2; Length 560;  
Best Local Similarity 26.0%; Pred. No. 6.4;  
Matches 27; Conservative 30; Mismatches 40; Indels 7; Gaps 2;  
QY 51 EACRDLRAVME--CRNTHLLOQLTEAOKGFQVDEAQAATGNTHTVMAASLDEKAG 108  
DB 185 ELRSDMSQIEQLNTLRH-----STKTELEKREKKAQSSSSMAEFNALAERAE 239  
QY 109 GOKVELEGEITTLNHLQDASAEVRLRENOVLSVRIADKK 152  
DB 240 NQRIKEIDPSATITQOKDIEALEKMKRVKKTITQRDER 283  
RESULT 11  
HCR\_PANPA STANDARD; PRT; 782 AA.  
ID HCR\_PANPA  
AC O8H57;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Alpha helical coiled-coil rod protein.  
GN Name=HCR;  
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.  
OX NCBI\_TaxID=9597;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Aasvalhti K., Kere J.;  
RT "HCR gene orthologs in chimpanzee, pygmy chimpanzee, gorilla, and  
RT orangutan.";  
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
CC -!- FUNCTION: May be a regulator of keratinocyte proliferation or  
CC differentiation (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL, AY135831; AAN12282.1; --  
CC EMBL, AY135815; AAN12282.1; JOINED.  
CC EMBL, AY135816; AAN12282.1; JOINED.  
CC EMBL, AY135817; AAN12282.1; JOINED.  
CC EMBL, AY135818; AAN12282.1; JOINED.  
CC EMBL, AY135819; AAN12282.1; JOINED.  
CC EMBL, AY135820; AAN12282.1; JOINED.  
CC EMBL, AY135821; AAN12282.1; JOINED.  
CC EMBL, AY135822; AAN12282.1; JOINED.  
CC EMBL, AY135823; AAN12282.1; JOINED.  
CC EMBL, AY135824; AAN12282.1; JOINED.  
CC EMBL, AY135825; AAN12282.1; JOINED.  
CC EMBL, AY135826; AAN12282.1; JOINED.

DR EMBL; AY135827; AANI2282.1; JOINED.  
 DR EMBL; AY135828; AANI2282.1; JOINED.  
 DR EMBL; AY135829; AANI2282.1; JOINED.  
 DR EMBL; AY135830; AANI2282.1; JOINED.  
 DR InterPro; IPR009800; HCR.  
 DR Pfam; PF07111; HCR; 1.  
 KW Coiled coil; Differentiation; Nuclear protein.  
 FT DOMAIN 82 314 Coiled coil (Potential).  
 FT DOMAIN 344 437 Coiled coil (Potential).  
 FT DOMAIN 498 691 Coiled coil (Potential).  
 SQ SEQUENCE 782 AA; 88668 MW; 6F07A52DA6741377 CRC64;

Query Match 12.2%; Score 104.5; DB 1; Length 782;  
 Best Local Similarity 25.3%; Pred. No. 9;  
 Matches 39; Conservative 32; Mismatches 44; Indels 39; Gaps 7;

QY 54 RDGLRAVME-----CRNYTHL---QDELTEAKGFQDVEAQ-AATC-----NHTYMA 97  
 DB 284 RSLQATVELLQVRVQSLTHIALQBEELTRKVPDSLEPFTRKCSQSLNRMREKVF 343  
 QY 98 LMASIDAEKAGQCKYBELBEGTITLNNK-----LQDASAEVERLRRENOV 143  
 DB 344 LMVQLKAQELHSDSVKQLKGVAQLQEVTSQSQEQAILQSLQDKAAEVERMGAG 403  
 QY 144 LSVRI-----ADKKYPPSSQDSSSAAPQLLIVL 172  
 DB 404 LQLELSRAQEARRRW-----QQOTASAEQRLIV 433

RESULT 12  
 HCR\_PANTR STANDARD; PRT; 782 AA.

AC OHZSO; OZYR47.  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Alpha helical coiled-coil rod protein.  
 GN Name=HCR;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Asumalani K., Kere J.;  
 RT "HCR gene orthologs in chimpanzee, pygmy chimpanzee, gorilla, and  
 RT orangutan."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;  
 RA Anzai T., Shilina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,  
 RA Yamagata T., Kulek J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,  
 RA Yamazaki M., Tashiro H., Iwamoto C., Umemura Y., Imanishi T.,  
 RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;  
 RT "Comparative sequencing of human and chimpanzee MHC class I regions  
 RT unveils insertions/deletions as the major path to genomic  
 RT divergence";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).  
 CC - FUNCTION: May be a regulator of keratinocyte proliferation or  
 CC differentiation (by similarity).  
 CC - SUBCELLULAR LOCATION: Nuclear and cytoplasmic (by similarity).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

CC EMBL; AY135777; AANI2279.1; -  
 DR EMBL; AY135761; AANI2279.1; JOINED.

DR EMBL; AY135762; AANI2279.1; JOINED.  
 DR EMBL; AY135763; AANI2279.1; JOINED.  
 DR EMBL; AY135764; AANI2279.1; JOINED.  
 DR EMBL; AY135765; AANI2279.1; JOINED.  
 DR EMBL; AY135766; AANI2279.1; JOINED.  
 DR EMBL; AY135767; AANI2279.1; JOINED.  
 DR EMBL; AY135768; AANI2279.1; JOINED.  
 DR EMBL; AY135769; AANI2279.1; JOINED.  
 DR EMBL; AY135770; AANI2279.1; JOINED.  
 DR EMBL; AY135771; AANI2279.1; JOINED.  
 DR EMBL; AY135772; AANI2279.1; JOINED.  
 DR EMBL; AY135773; AANI2279.1; JOINED.  
 DR EMBL; AY135774; AANI2279.1; JOINED.  
 DR EMBL; AY135775; AANI2279.1; JOINED.  
 DR EMBL; AY135776; AANI2279.1; JOINED.  
 DR EMBL; AB100083; BAC78167.1; ALT\_INIT.  
 DR InterPro; IPR009800; HCR.  
 DR Pfam; PF07111; HCR; 1.  
 KW Coiled coil; Differentiation; Nuclear protein.  
 FT DOMAIN 82 314 Coiled coil (Potential).  
 FT DOMAIN 344 437 Coiled coil (Potential).  
 FT DOMAIN 498 691 Coiled coil (Potential).  
 FT DOMAIN 671 871 Coiled coil (Potential).  
 FT CONFLICT 288 388 O -> H (in Ref. 2).  
 FT CONFLICT 319 329 S -> T (in Ref. 2).  
 FT CONFLICT 638 639 R -> H (in Ref. 2).  
 FT CONFLICT 671 671 R -> Q (in Ref. 2).  
 SQ SEQUENCE 782 AA; 88660 MW; D140F8587129D054 CRC64;

Query Match 12.2%; Score 104.5; DB 1; Length 782;  
 Best Local Similarity 25.3%; Pred. No. 9;  
 Matches 39; Conservative 32; Mismatches 44; Indels 39; Gaps 7;

QY 54 RDGLRAVME-----CRNYTHL---QDELTEAKGFQDVEAQ-AATC-----NHTYMA 97  
 DB 284 RSLQATVELLQVRVQSLTHIALQBEELTRKVPDSLEPFTRKCSQSLNRMREKVF 343  
 QY 98 LMASIDAEKAGQCKYBELBEGTITLNNK-----LQDASAEVERLRRENOV 143  
 DB 344 LMVQLKAQELHSDSVKQLKGVAQLQEVTSQSQEQAILQSLQDKAAEVERMGAG 403  
 QY 144 LSVRI-----ADKKYPPSSQDSSSAAPQLLIVL 172  
 DB 404 LQLELSRAQEARRRW-----QQOTASAEQRLIV 433

## RESULT 13

Q7R6H3 PRELIMINARY; PRT; 900 AA.

AC Q7R6H3;  
 DT 01-MAR-2004 (TREMBlrel. 26, Created)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE GIP 170.182668.185370.  
 DE Giardia lamblia ATCC 50803.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
 OX NCBI\_TaxID=184922;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WB C6;  
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 RA Olsen G.J., Sogin M.L.;  
 RL "Draft sequence of the Giardia lamblia genome."  
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC - CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AACB01000001; EAA43024.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN 1.  
 SQ SEQUENCE 900 AA; 103880 MW; 72339FBCACCA19 CRC64;

Query Match 12.2%; Score 104; DB 2; Length 900;  
 Best Local Similarity 30.7%; Pred. No. 11;

	Matches	39;	Conservative	19;	Mismatches	47;	Indels	22;	Gaps	5
Qy	43	IFTTAKN-SEACRDLRAVMECRNVTYHLLQELTEAQKGFQDVEAQATCNHTNALMAS	101							
Db	295	IHKLKADISEANROSTNNSSNAEKETOIQOHLEAAQ----	ARAEAAQAQTLNLSQSK	350						
Qy	102	LDA--EKAQOKKYVEELLEGELT-----	TLNHLQDASAEVETLRRENO-----	VL	144					
Db	351	LDSLEIAGHNTTEEKVEQLKQGLTOAQEOLKQIKHENNEIGREHDLSPRAQVGRSLHYA	410							
Qy	145	SVRIADK	151							
Db	411	QVSIAADK	417							

**This Page Blank (uspto)**